

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:17:08 ; Search time 153.792 Seconds
(without alignments)
791.381 Million cell updates/sec

Title: US-10-029-926d-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAGALLLAQA.....VLGAARQLISEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1440	100.0	277	5	ABG78150 Human Fv
2	1440	100.0	277	5	ABG91841 Human ant
3	1436	99.7	277	8	Adi28366 Human scf
4	1436	99.7	277	8	AdS82026 Human pla
5	1416	98.3	277	5	ABG78328 Human Fv
6	1416	98.3	277	5	ABG92019 Human ant
7	1397.5	97.0	278	8	Adi28367 Human scf
8	1397.5	97.0	278	8	AdS82027 Human pla
9	1393.5	96.8	280	8	AdJ57363 P-selecti
10	1393.5	96.8	280	8	AdC63078 Human scf
11	1388.5	96.4	280	9	AdX01131 Amino aci
12	1388.5	96.4	280	9	AdY78325 Single ch
13	1386.5	96.3	280	8	Adi28368 Human scf
14	1386.5	96.3	280	8	AdS82028 Human leu
15	1379.5	95.8	280	9	AdX01181 Amino aci
16	1379.5	95.8	280	9	AdX01130 Amino aci
17	1379.5	95.8	280	9	AdY78324 Single ch
18	1379.5	95.8	280	9	AdY78375 Single ch
19	1378.5	95.7	280	9	AdX01185 Amino aci
20	1378.5	95.7	280	9	AdY78379 Single ch
21	1378	95.7	266	5	ABG92020 Human ant
22	1375.5	95.5	280	9	AdX01186 Amino aci
23	1375.5	95.5	280	9	AdY78380 Single ch
24	1374.5	95.5	280	9	AdX01180 Amino aci

25	1374.5	95.5	280	9	ADY78374
26	1294	89.9	291	8	ADN06989
27	1278.5	88.8	282	4	AAE02185
28	1275.5	88.6	309	2	AAW83322
29	1275.5	88.6	309	5	ABB09603
30	1275.5	88.6	309	6	ABG74384
31	1275.5	88.6	309	7	ADG98737
32	1275.5	88.6	309	8	ADO40446
33	1257	87.3	246	5	ABG78329
34	1257	87.3	246	5	ABG92026
35	1250	86.8	256	5	ABG78334
36	1250	86.8	256	5	ABG92025
37	1240	86.1	244	9	ADW90315
38	1240	86.1	244	9	ADX01815
39	1231.5	85.5	260	5	ABG92023
40	1223	84.9	263	5	ABG92024
41	1218.5	84.6	239	5	ABP44926
42	1218.5	84.6	239	7	ADG95753
43	1212.5	84.2	239	5	ABP46027
44	1212.5	84.2	239	7	ADG96854
45	1201.5	83.4	290	6	ABP55318

ALIGNMENTS

RESULT 1

ABG78150

ID ABG78150 standard; protein; 277 AA.

XX AC ABG78150;

XX AC

DT 15-NOV-2002 (first entry)

XX XX

DE Human Fv molecule hypervariable region related peptide #25.

XX XX

KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX KW

OS Homo sapiens.

XX OS

FN WO200259264-A2.

XX FN

PD 01-AUG-2002.

XX PD

PF 31-DEC-2001; 2001WO-US049440.

XX PF

PR 29-DEC-2000; 2000US-00751181.

XX PR

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PA

FI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A; Plaksin D, Peretz T;

XX FI

DR WPI; 2002-619166/66.

XX DR

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other cells.

XX PT

PS Claim 4; Page 155-156; 232pp; English.

XX PS

CC The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

XX
 SQ Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 5.2e-89;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQAPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGM5WVR 60
 DB 1 MKYLLPTAAAGLLLLAAQAPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGM5WVR 60
 QY 61 QAPKGLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 DB 61 QAPKGLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 QY 121 MRAPVIWGQGLTVTVSRGG 180
 DB 121 MRAPVIWGQGLTVTVSRGG 180
 QY 181 YYASWYQQKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNS 240
 DB 181 YYASWYQQKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNS 240
 QY 241 RDSGNGHVVFGGTKLTVLGAABEQKLISEEDLNGAA 277
 DB 241 RDSGNGHVVFGGTKLTVLGAABEQKLISEEDLNGAA 277

RESULT 2
 ABG91841

ID ABG91841 standard; protein; 277 AA.

XX AC ABG91841;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #25.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-67476/72.

XX FT Novel isolated epitope present on cancer cells and important in
 FT physiological phenomena such as cell rolling, metastasis and
 FT inflammation, for treating autoimmune, inflammatory or cardiovascular
 FT diseases, and cancer.

XX

PS Claim 23; Page 233-234; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

XX SQ Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 5.2e-89;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQAPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGM5WVR 60
 DB 1 MKYLLPTAAAGLLLLAAQAPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGM5WVR 60
 QY 61 QAPKGLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 DB 61 QAPKGLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYCAR 120
 QY 121 MRAPVIWGQGLTVTVSRGG 180
 DB 121 MRAPVIWGQGLTVTVSRGG 180
 QY 181 YYASWYQQKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNS 240
 DB 181 YYASWYQQKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNS 240
 QY 241 RDSGNGHVVFGGTKLTVLGAABEQKLISEEDLNGAA 277
 DB 241 RDSGNGHVVFGGTKLTVLGAABEQKLISEEDLNGAA 277

RESULT 3

AD128366

ID AD128366 standard; protein; 277 AA.

XX AC AD128366;

XX DT 06-MAY-2004 (first entry)

XX DE Human scFv fragment Y1, binds to platelets.

XX KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

XX OS Homo sapiens.

XX PN WO2004002528-A1.

XX PD 08-JAN-2004.

XX PF 30-JUN-2003; 2003WO-US020604.

XX PR 01-JUL-2002; 2002US-00189025.

(SAVI-) SAVIENT PHARM INC.

Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

WPI; 2004-099189/10.

Composition comprising an agent and/or antibody or its fragment, useful for treating auto-immune disease, thrombosis, restenosis, metastasis, or for inhibiting growth and/or replication of tumor cells or leukemia cells.

Claim 13; SEQ ID NO 1; 58pp; English.

The present sequence is the protein sequence of human scFv fragment Y1. This antibody was identified by screening a human antibody phage library that has diversity only in the heavy chain CDR3 regions. Fixed human platelets were screened in order to identify antibodies that bind platelets. The epitope for Y1 antibody is located between amino acids 272 and 285 on glycoalbumin, a subunit of the CD42 complex. Y1 also binds the N-terminal of PSEL-1, a receptor for E-, L- and P-selectins, and has a high affinity for primary leukemia cells. The invention relates to compositions utilizing an agent and an antibody or its fragment. The agent is a toxin, radioisotope or pharmaceutical agent such as doxorubicin. It is complexed or combined with or conjugated to the antibody or its fragment. The agent and/or antibody can be present in the composition as a sub-clinical amount, i.e. less than the amount generally found to be clinically effective when the agent is administered alone. The composition is used in claimed methods of: inhibiting cell rolling, inflammation, thrombosis, restenosis, metastasis, the growth and/or replication of tumor cells or leukemia cells, an increase in number of tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet complex formation, aggregation or adhesion; increasing the mortality rate of tumor or leukemia cells, the susceptibility of disease cells to damage by anti-disease agents, and the susceptibility of tumor or leukemia cells to damage by anti-cancer agents; and ameliorating the effects of a disease, preventing a disease, treating a disease or inhibiting the progress of a disease.

Sequence 277 AA;

Query Match 99.7%; Score 1436; DB 8; Length 277;

Best Local Similarity 99.6%; Pred. No. 9.6e-89;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MKYLLPTAAAGLLLLAAQAPMAEVQVVGSGGVVVRPGGSLRLSCAASGFTDDYGMWVR 60

1 MKYLLPTAAAGLLLLAAQAPMAEVQVVGSGGVVVRPGGSLRLSCAASGFTDDYGMWVR 60

61 QAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

61 QAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

121 MRAPVINGQGLTVTVSRGGGSGGGGGSSSELTPDPAVSVALGQTVRITCGDSLRS 180

121 MRAPVINGQGLTVTVSRGGGSGGGGGSSSELTPDPAVSVALGQTVRITCGDSLRS 180

181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240

181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240

241 RDSSGNHVFVGGGKTLTVLGAARFQKLI SEEDLNGAA 277

241 RDSSGNHVFVGGGKTLTVLGAARFQKLI SEEDLNGAA 277

RESULT 4

ADSS82026

ID ADS82026 standard; protein; 277 AA.

XX

AC

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DT

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Human platelet binding scFv antibody fragment Y1.

cell rolling; inflammation; autoimmune disease; thrombosis; restenosis; metastasis; tumour; leukaemia; cardiovascular disease; retinopathy; human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic; vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.

Homo sapiens.

US2004202665-A1.

14-OCT-2004.

30-JUN-2003; 2003US-00610843.

01-JUL-2002; 2002US-0393453P.

(LAZA/) LAZAROVITS J.

(NIMR/) NIMROD A.

(HOCH/) HOCH M H.

(LEVA/) LEVANON A.

Lazarovits J, Nimrod A, Hoch MH, Levanon A;

WPI; 2004-746943/73.

Composition useful for treating diseases e.g., inflammatory diseases, thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or retinopathic diseases, comprises agent and antibody or its fragment.

Claim 13; SEQ ID NO 1; 22pp; English.

The invention relates to a composition which comprises an agent and an antibody or its fragment. The composition is useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet complex formation, aggregation or adhesion, increase in number of tumour cells or growth and/or replication of tumour or leukemia cells, for increasing the mortality rate of tumour or leukemia cells, the susceptibility of tumour or leukemia cells to damage by anti-cancer agents, for decreasing number of tumour or leukemia cells, or for ameliorating the effect of a disease, preventing a disease, treating a disease, or inhibiting the progress of a disease. The composition is useful for therapeutic treatment, where antibody or its fragment and the agent are administered separately. The antibody or its fragment is administered prior to or subsequent to the agent. The composition is useful for treating diseases such as inflammatory diseases, diseases involving abnormal or pathogenic adhesion, thrombosis and/or restenosis, diseases involving abnormal or pathogenic aggregation, autoimmune diseases, cardiovascular diseases, retinopathic diseases, diseases caused by sulphated tyrosine-dependent protein-protein interactions or diseased cells. The present sequence represents the human platelet binding scFv antibody fragment Y1.

Sequence 277 AA;

Query Match 99.7%; Score 1436; DB 8; Length 277;

Best Local Similarity 99.6%; Pred. No. 9.6e-89;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MKYLLPTAAAGLLLLAAQAPMAEVQVVGSGGVVVRPGGSLRLSCAASGFTDDYGMWVR 60

1 MKYLLPTAAAGLLLLAAQAPMAEVQVVGSGGVVVRPGGSLRLSCAASGFTDDYGMWVR 60

61 QAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

61 QAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR 120

121 MRAPVINGQGLTVTVSRGGGSGGGGGSSSELTPDPAVSVALGQTVRITCGDSLRS 180

121 MRAPVINGQGLTVTVSRGGGSGGGGGSSSELTPDPAVSVALGQTVRITCGDSLRS 180

181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240

CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 277 AA;

Query Match 98.3%; Score 1416; DB 5; Length 277;
 Best Local Similarity 98.2%; Pred. No. 2.1e-87;
 Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDDYGMWVR 60
 Db |||||
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDDYGMWVR 60
 Db |||||
 Qy 61 QAPGKGLVWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
 Db |||||
 Qy 61 QAPGKGLVWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
 Qy 121 MRAPVINGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
 Db : |||||
 Qy 121 LTHPYFGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRS 180
 Qy 181 YYASWYQKPGQAPVLIYGNKRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
 Db |||||
 Qy 181 YYASWYQKPGQAPVLIYGNKRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
 Qy 241 RDSGSGNHVFGGKTLTVLGAABQKLISEEDLNGAA 277
 Db 241 RDSGSGNHVFGGKTLTVLGAABQKLISEEDLNGAA 277

RESULT 7

AD128367
 ID AD128367 standard; protein; 278 AA.
 XX
 AC AD128367; .
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment Y17, binds to platelets.
 XX
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020604.
 XX
 PR 01-JUL-2002; 2002US-00189025.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 XX
 DR WPI; 2004-099189/10.
 XX

Composition comprising an agent and/or antibody or its fragment, useful
 for treating auto-immune disease, thrombosis, restenosis, metastasis, or
 for inhibiting growth and/or replication of tumor cells or leukemia
 cells.

Claim 13; SEQ ID NO 2; 58pp; English.

The present sequence is the protein sequence of human scFv fragment Y17.
 This antibody was identified by screening a human antibody phage library
 that has diversity only in the heavy chain CDR3 regions. Fixed human
 platelets were screened in order to identify antibodies that bind

CC platelets. Y17 binds leukaemic cells. The invention relates to
 CC compositions utilising an agent and an antibody or its fragment. The
 CC agent is a toxin, radioisotope or pharmaceutical agent such as
 CC doxorubicin. It is complexed or combined with or conjugated to the
 CC antibody or its fragment. The agent and/or antibody can be present in the
 CC composition is a sub-clinical amount, i.e. less than the amount generally
 CC found to be clinically effective when the agent is administered alone.
 CC The composition is used in claimed methods of: inhibiting cell rolling,
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
 CC replication of tumour cells or leukaemia cells, an increase in number of
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
 CC susceptibility of disease cells to damage by anti-disease agents, and the
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
 CC agents; and ameliorating the effects of a disease, preventing a disease,
 CC treating a disease or inhibiting the progress of a disease.

XX Sequence 278 AA;

Query Match 97.0%; Score 1397.5; DB 8; Length 278;
 Best Local Similarity 97.8%; Pred. No. 3.8e-86;
 Matches 272; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD-DYGMWV 59
 Db |||||
 Qy 60 RQAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCA 119
 Db |||||
 Qy 61 RQAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCA 120
 Qy 120 RMRAPVINGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRL 179
 Db |||||
 Qy 121 RMRAPVINGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVAGTQVTRITCGDSLRL 180
 Qy 180 SYTASWYQKPGQAPVLIYGNKRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCN 239
 Db |||||
 Qy 181 SYTASWYQKPGQAPVLIYGNKRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCN 240
 Qy 240 RDSGSGNHVFGGKTLTVLGAABQKLISEEDLNGAA 277
 Db 241 RDSGSGNHVFGGKTLTVLGAABQKLISEEDLNGAA 278

RESULT 8

ADS82027
 ID ADS82027 standard; protein; 278 AA.
 XX
 AC ADS82027;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Human platelet binding scFv antibody fragment Y17.
 XX
 KW cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
 KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
 KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;
 KW vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.
 XX
 OS Homo sapiens.
 XX
 PN US20040202665-A1.
 XX
 PD 14-OCT-2004.
 XX
 PF 30-JUN-2003; 2003US-00610843.
 XX
 PR 01-JUL-2002; 2002US-0393453P.
 XX
 PA (LAZA/) LAZAROVITS J.
 XX (NIMR/) NIMROD A.
 PA (HOCH/) HOCH M H.

PA (LEVA/) LEVANON A.
XX Lazarovits J, Nimrod A, Hoch MH, Levanon A;
XX MPI; 2004-746943/73.
XX
XX Composition useful for treating diseases e.g., inflammatory diseases,
PT thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
PT retinopathic diseases, comprises agent and antibody or its fragment.
XX
XX Claim 13; SEQ ID NO 2; 22pp; English.
XX
XX The invention relates to a composition which comprises an agent and an
CC antibody of its fragment. The composition is useful for inhibiting cell
CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
CC and/or cell-platelet complex formation, aggregation or adhesion, increase
CC in number of tumour cells or growth and/or replication of tumour or
CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
CC ameliorating the effect of a disease, preventing a disease, treating a
CC disease, or inhibiting the progress of a disease. The composition is
CC useful for therapeutic treatment, where antibody or its fragment and the
CC agent are administered separately. The antibody or its fragment is
CC administered prior to or subsequent to the agent. The composition is
CC useful for treating diseases such as inflammatory diseases, diseases
CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
CC diseases involving abnormal or pathogenic aggregation, autoimmune
CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
CC by sulphated tyrosine-dependent protein-protein interactions or diseased
CC cells. The present sequence represents the human platelet binding scFv
CC antibody fragment Y17.
XX
XX Sequence 278 AA;
XX
Query Match 97.0%; Score 1397.5; DB 8; Length 278;
Best Local Similarity 97.8%; Pred. No. 3.8e-85; Indels 1; Gaps 1;
Matches 272; Conservative 1; Mismatches 4;
QY 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD-DYGMSSW 59
DB 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLTHPFW 60
QY 60 RQAPGKLEWVSGINWNGSTGADSVKGRFTISRDNAKNSLYLQMSLRAEDTAVYCA 119
DB 61 RQAPGKLEWVSGINWNGSTGADSVKGRFTISRDNAKNSLYLQMSLRAEDTAVYCA 120
QY 120 RMRAPVWGQGLTVVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179
DB 121 RMRAPVWGQGLTVVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 180 SYVASWYQQKPGAPLVLYYKNNRPSGIPDRFSGSSSGNTASITITGAQAEADYYCN 239
DB 181 SYVASWYQQKPGAPLVLYYKNNRPSGIPDRFSGSSSGNTASITITGAQAEADYYCN 240
QY 240 SRDSSGNHVVFGGQTKLVTLGAABEQKLISEEDINGAA 277
DB 241 SRDSSGNHVVFGGQTKLVTLGAABEQKLISEEDINGAA 278
RESULT 9
ID ADJ57363 standard; protein; 280 AA.
XX
XX ADJ57363;
XX
XX ADJ57363;
DT 06-MAY-2004 (first entry)
XX
XX P-selectin glycoprotein ligand-1-binding scFv antibody fragment I32.
DE
XX P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;
XX antiinflammatory; immunosuppressive; human.
KW
KW
OS Homo sapiens.
XX Key Location/Qualifiers
FH Region 53..60
FT /label= CDR1
FT /note= "Specifically referred to in Claim 2"
PT 75..90
FT /label= CDR2
FT /note= "Specifically referred to in Claim 2"
FT 124..129
FT /label= CDR3
FT /note= "Specifically referred to in Claim 2"
XX WO2004003166-A2.
XX 08-JAN-2004.
XX 30-JUN-2003; 2003WO-US020602.
XX 01-JUL-2002; 2002US-00189032.
XX (SAVI-) SAVIENT PHARM INC.
XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
PI Hoch Mar- Chaim H;
PI MPI; 2004-203378/19.
XX
XX Novel antibody or its fragment that binds to an epitope of P-Selectin-
PT Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,
PT infection, auto-immune disease, metastasis, tumor/leukemia cell in
PT patient.
XX
XX Claim 1; SEQ ID NO 1; 106pp; English.
XX
XX The present sequence is that of an scFv antibody fragment, designated
CC L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody
CC was identified by screening a phage library, which had diversity only in
CC the heavy chain CDR3 regions, against a leukaemia cell to select specific
CC antibodies that recognised leukaemia cell surface determinants, wherein
CC the specific receptor was not previously known or characterised. The
CC invention relates to an antibody or its fragment having the binding
CC capabilities of L32. Such antibodies can be used in therapeutic,
CC diagnostic, prognostic and staging methods. Pharmaceutical compositions
CC comprising such antibodies are used to treat conditions related to:
CC inhibiting or treating cell rolling, inflammation, autoimmune disease,
CC infection (e.g. HIV infection), metastasis, and growth and/or replication
CC of tumour cells; increasing the mortality of tumour cells; inhibiting
CC growth and/or replication of tumour cells; inhibiting growth and/or
CC replication of leukaemia cells; increasing the mortality rate of
CC leukaemia cells; altering the susceptibility of diseased cells to damage
CC by anti-disease agents; increasing the susceptibility of tumour cells to
CC damage by anti-cancer agents; increasing the susceptibility of leukaemia
CC cells to damage by anti-leukaemia agents; inhibiting increase in number
CC of tumour cells in a patient; decreasing the number of tumour cells in a
CC patient; inhibiting increase in number of leukaemia cells in a patient;
CC and decreasing the number of leukaemic cells in a patient. Other methods
CC are provided to induce antibody-dependent cell-mediated cytotoxicity or
CC stimulate natural killer or T cells using the antibodies. A method of
CC purging tumour cells from a patient involves incubating the cells with
CC the antibody.
XX
XX Sequence 280 AA;
XX
Query Match 96.8%; Score 1393.5; DB 8; Length 280;
Best Local Similarity 97.1%; Pred. No. 7e-86; Indels 3; Gaps 1;
Matches 272; Conservative 0; Mismatches 5;
QY 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD---DYGMS 57
DB 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLNPVKHM 60

Qy 58 WVRQAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRADTVAVY 117
 Db 61 WVRQAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRADTVAVY 120
 Qy 118 CARMRAPVINGQGTIVTVSRGGGSGGGGSGGSELTPDPAVSVALGOTVTRITCOGDS 177
 Db 121 CARMRAPVINGQGTIVTVSRGGGSGGGGSGGSELTPDPAVSVALGOTVTRITCOGDS 180
 Qy 178 LRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYY 237
 Db 181 LRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYY 240
 Qy 238 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 277
 Db 241 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 280

RESULT 10
 ADT63078
 ID ADT63078 standard; protein; 280 AA.
 AC ADT63078;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human scFv antibody fragment binding PSGL-1.
 XX
 KW P-selectin Glycoprotein Ligand-1; PSGL-1; heavy chain;
 KW complementarity determining region; CDR;
 KW T cell-acute lymphoblastic leukaemia cell;
 KW acute myelogenous leukaemia' cell; B-leukaemia cell;
 KW B cell-chronic lymphocytic leukaemia; multiple myeloma cell;
 KW tumour cell; anti-cancer; cytostatic; anti-immune disease; metastasis;
 KW inflammation; HIV infection; auto-immune disease; inflammatory;
 KW immunosuppressive; anti-HIV; human; scFv antibody fragment.
 XX
 OS Homo sapiens.
 XX
 PN US2004208877-A1.
 XX
 PD 21-OCT-2004.
 XX
 PF 30-JUN-2003; 2003US-00611588.
 XX
 PR 01-JUL-2002; 2002US-0393491P.
 XX
 PA (LEVA/) LEVANON A.
 PA (BENL/) BEN-LEVY R.
 PA (PLAK/) PLAKSIN D.
 PA (SZAN/) SZANTON E.
 PA (HAGA/) HAGAI Y.
 PA (MARC/) MAR-CHAIM H H.
 XX
 PI Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
 PI Mar-Chaim HH;
 PI
 XX
 WPI; 2004-765453/75.
 XX
 PT New antibody or its fragment that binds to an epitope of P-selectin
 PT Glycoprotein Ligand-1 (PSGL-1), useful for manufacturing a medicament for
 PT treating e.g., inflammation, HIV infection, auto-immune disease, and
 PT metastasis.
 XX
 PS Claim 1; SEQ ID NO 1; 49pp; English.
 XX
 CC The present invention relates to an antibody or its fragment that binds
 CC to an epitope of P-selectin Glycoprotein Ligand-1 (PSGL-1) comprising a
 CC sequence comprising 280 amino acids (SEQ ID NO: 1) fully defined in the
 CC specification, that has the binding capabilities of an scFv of SEQ ID NO:
 CC 1, or comprising one heavy chain complementarity determining region
 CC (CDR). The heavy chain CDR comprises the sequences given in the
 CC specification as SEQ ID NO: 2, 3, or 4. Two or three heavy chain CDRs are
 CC selected from SEQ ID NO: 2, 3, and 4. The antibody or its fragment

CC comprises at least one framework variable region from germline DP32. It
 CC may be a substantially circular or looped peptide or polypeptide. The
 CC epitope comprises at least one sulphated moiety. The antibody or its
 CC fragment may bind or cross-react with two or more epitopes, each epitope
 CC comprising one or more sulphated tyrosine residues, preferably comprising
 CC at least one cluster of two or more acidic amino acids. It may bind to an
 CC epitope on at least one cell selected from T cell-acute lymphoblastic
 CC leukaemia cells, acute myelogenous leukaemia cells, B-leukaemia cells, B
 CC cell-chronic lymphocytic leukaemia, and multiple myeloma cells. It may
 CC bind to an epitope on a lipid, carbohydrate, peptide glycolipid,
 CC glycoprotein, lipoprotein, and/or lipopolysaccharide molecule. It may be
 CC coupled to a complex with an agent selected from anti-cancer, anti-
 CC leukemic, anti-metastasis, anti-neoplastic, anti-disease, anti-adhesion,
 CC anti-thrombosis, anti-restenosis, anti-autoimmune, anti-aggregation, anti-
 CC bacterial, anti-viral, and anti-inflammatory agents, preferably anti-
 CC viral agent selected from acyclovir, ganciclovir and zidovudine. The
 CC agent may be selected from toxins, radioisotopes, imaging agents, and
 CC pharmaceutical agents. The antibody or its fragment may be coupled to or
 CC complexed with a vehicle or carrier that can be coupled or complexed to
 CC more than one agent. The vehicle or carrier is selected from dextran,
 CC lipophilic polymers, HPMA, and liposomes, and their derivatives and
 CC modifications. A pharmaceutical composition comprising the antibody or
 CC its fragments is useful in a method for treating a disease or cell
 CC rolling in a patient, for ameliorating the effects of inflammation,
 CC preventing inflammation, treating inflammation, or inhibiting the
 CC progress of inflammation, for treating an infection, i.e. caused by HIV,
 CC where the administration prevents cell entry of HIV, for treating an auto-
 CC immune disease, for treating metastasis, or for treating growth and/or
 CC replication of tumour or leukaemia cells. The pharmaceutical composition
 CC is also useful for manufacturing a medicament for treating the diseases.
 CC The pharmaceutical composition is useful for increasing the mortality
 CC rate of tumour or leukaemia cells, altering the susceptibility of
 CC diseased, tumour or leukaemia cells to damage by anti-disease agents or
 CC anti-cancer agents, inhibiting increase in number or decreasing number of
 CC tumour or leukaemia cells in a patient having a tumour or leukaemia,
 CC eliciting antibody dependent cell-mediated cytotoxicity or stimulating a
 CC natural killer cell or a T cell, diagnosing, prognosing or staging a
 CC metastasis, tumour cell, or leukaemia in a patient, or for purging tumour
 CC cells from a patient. The present sequence represents a human scFv
 CC antibody fragment that binds to an epitope of PSGL-1.
 XX
 SQ Sequence 280 AA;

Query Match 96.8%; Score 1393.5; DB 8; Length 280;
 Best Local Similarity 97.1%; Pred. No. 7e-86;
 Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
 Qy 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVESGQGVVRRPGSLRLSCAASGFTFD---DYGMS 57
 Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQLVESGQGVVRRPGSLRLSCAASGFTFDLNPVKHM 60
 Qy 58 WVRQAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRADTVAVY 117
 Db 61 WVRQAPKGLWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRADTVAVY 120
 Qy 118 CARMRAPVINGQGTIVTVSRGGGSGGGGSGGSELTPDPAVSVALGOTVTRITCOGDS 177
 Db 121 CARMRAPVINGQGTIVTVSRGGGSGGGGSGGSELTPDPAVSVALGOTVTRITCOGDS 180
 Qy 178 LRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYY 237
 Db 181 LRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYY 240
 Qy 238 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 277
 Db 241 CNSRDSGNHVVFGGKTLTVLGAARQKLISEEDLNGAA 280

RESULT 11
 ADX01131
 ID ADX01131 standard; protein; 280 AA.
 XX
 AC ADX01131;

CC The invention relates to an antibody or its fragment (I) comprising the
CC consensus sequence X1-X2-X3-Pro-X5-X6, where X1 and X6 are hydrophobic
CC amino acids and X2, X3 and X5 are any amino acid. Also described: (1) a
CC pharmaceutical composition (II), comprising (I) and a carrier; (2) a
CC diagnostic, prognostic, or staging kit (K1), comprising (I) and an
CC imaging agent; (3) an isolated or purified DNA sequence (III) encoding
CC host cell (V) comprising (IV) comprising (III); (5) a recombinant
CC immunoglobulin binding domain, comprising (I); (7) a library (VII) of
CC domain for complementary binding, where (VII) has diversity only in heavy
CC chain CDR3; (8) a small inorganic molecule (VIII) capable of binding to a
CC sulfated epitope of PSG1-1, GF1b, and/or CCR5; and (9) a pharmaceutical
CC composition (IX), comprising (VIII). (II) is useful for treating a
CC disease, cell rolling, an infection (where the infection is caused by HIV
CC and the administration of (II) prevents entry of HIV), and inflammation.
CC (II) can also be used for inhibiting autoimmune disease, inhibiting
CC metastasis, inhibiting growth and/or replication of tumor cells, and/or
CC increasing the mortality rate of tumor cells, inhibiting growth and/or
CC replication of leukemia cells, increasing the mortality rate of leukemia
CC cells, inhibiting growth and/or replication of B-CLL cells, altering the
CC susceptibility of diseased cells to damage by anti-cancer agents,
CC increasing the susceptibility of leukemia cells to damage by anti-
CC leukemia agents, increasing the susceptibility of B-CLL cells to damage
CC by anti-leukemia agents, inhibiting platelet aggregation, inhibiting
CC restenosis, eliciting antibody dependent cell-mediated cytotoxicity
CC (ADCC) mediated by effector cells comprising of natural killer (NK) or
CC monocytic cells), eliciting apoptosis in leukemia cells, stimulating a NK
CC cell or a T cell, and manufacturing medicament for treating a disease.
CC (I) is useful for diagnosing, prognosing or staging a disease in a
CC patient, which involves providing a sample containing a cell from the
CC patient and determining whether (I) binds to the cell of the patient, and
CC so indicates that the patient is at risk for or has the disease. (I) is
CC useful for purging tumor cells from a patient, which involves providing a
CC sample containing cells from the patient and incubating the cells from
CC the patient with (I), where the purging occurs ex vivo. (VII) is useful
CC for selecting a sulfated epitope, which involves providing (VII), panning
CC (VII) for a sulfated epitope that binds to the antigen binding domain,
CC and isolating the sulfated epitope. (V) is useful for producing (I). (II)
CC is useful for treating cardiovascular diseases such as myocardial
CC infarction and inflammatory diseases. The present sequence represents a
CC scfv antibody from the present invention.

XX Sequence 280 AA;

Query Match 96.4%; Score 1388.5; DB 9; Length 280;
Best Local Similarity 96.8%; Pred. No. 1.5e-85;
Matches 271, Conservative 0; Mismatches 6; Indels 3; Gaps 1;
Qy 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD---DYGMS 57
Db 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLNPVKVHM 60
Qy 58 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAVY 117
Db 61 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAVY 120
Qy 118 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGOTVTRITCGDS 177
Db 121 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGOTVTRITCGDS 180
Qy 178 LRSYASWYQKPGQAPVLYVIGNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237
Db 181 LRSYASWYQKPGQAPVLYVIGNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 240
Qy 238 CNSRDSGNHVVFGGKTLVLGAAAEQKLISEEDINGAA 277
Db 241 CNSRDSGNHVVFGGKTLVLGAAAEQKLISEEDINGAA 280

RESULT 13

ADI28368

ID ADI28368 standard; protein; 280 AA.

XX

AC ADI28368;

XX DT 06-MAY-2004 (first entry)

XX DE Human scFv fragment L32, binds to leukaemia cells.

XX KW Human; antibody; scFv; leukaemia; drug delivery; cancer; therapy.

XX OS Homo sapiens.

XX PN W02004002528-A1.

XX PD 08-JAN-2004.

XX PF 30-JUN-2003; 2003WO-US020604.

XX PR 01-JUL-2002; 2002US-00189025.

XX PA (SAVI-) SAVIENT PHARM INC.

XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

XX DR WPI; 2004-099189/10.

XX Composition comprising an agent and/or antibody or its fragment, useful
XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or
XX for inhibiting growth and/or replication of tumor cells or leukemia
XX cells.

PS Claim 13; SEQ ID NO 3; 58pp; English.

XX The present sequence is the protein sequence of human scFv fragment L32.
XX This antibody was identified by screening a human antibody phage library
XX that has diversity only in the heavy chain CDR3 regions. Leukemia cells
XX were screened to select specific antibodies that recognise leukemia cells
XX surface determinants. The invention relates to compositions utilising an
XX agent and an antibody or its fragment. The agent is a toxin, radioisotope
XX or pharmaceutical agent such as doxorubicin. It is complexed or combined
XX with or conjugated to the antibody or its fragment. The agent and/or
XX antibody can be present in the composition is a sub-clinical amount, i.e.
XX less than the amount generally found to be clinically effective when the
XX agent is administered alone. The composition is used in claimed methods
XX of: inhibiting cell rolling, inflammation, thrombosis, restenosis,
XX metastasis, the growth and/or replication of tumor cells or leukemia
XX cells, an increase in number of tumor or leukemia cells, cell-cell,
XX cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet
XX complex formation, aggregation or adhesion; increasing the mortality rate
XX of tumor or leukemia cells, the susceptibility of disease cells to
XX damage by anti-disease agents, and the susceptibility of tumor or
XX leukemia cells to damage by anti-cancer agents; and ameliorating the
XX effects of a disease, preventing a disease, creating a disease or
XX inhibiting the progress of a disease.

XX Sequence 280 AA;

Query Match 96.3%; Score 1386.5; DB 8; Length 280;
Best Local Similarity 96.8%; Pred. No. 2.1e-85;
Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

Qy 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFD---DYGMS 57
Db 1 MKYLLPTAAAGLLLLAQAQPAEAQVQLVSGGVRPGGSLRLSCAASGFTFDLNPVKVHM 60
Qy 58 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAVY 117
Db 61 WYQAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNAKNSLYLQNSLRADTVAVY 120
Qy 118 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGOTVTRITCGDS 177
Db 121 CARMRAPVWGQGTFLVTVSRGGSGGGGGSSSELTQDPVAVSVALGOTVTRITCGDS 180
Qy 178 LRSYASWYQKPGQAPVLYVIGNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237
|||

Db 181 LRSYASWYQKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240

QY 238 CNSRDSSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277

Db 241 CNSRDSSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 280

RESULT 14

ADS82028

ID ADS82028 standard; protein; 280 AA.

XX AC ADS82028;

XX DT 30-DEC-2004 (first entry)

XX Human leukaemia cell binding scFv antibody fragment L32.

XX cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;

KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;

KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;

KW vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.

XX Homo sapiens.

XX US2004202665-A1.

XX PD 14-OCT-2004.

XX 30-JUN-2003; 2003US-00610843.

XX PF 01-JUL-2002; 2002US-0393453P.

XX PA (LAZA/) LAZAROVITS J.

XX PA (NIMR/) NIMROD A.

XX PA (HOCH/) HOCH M H.

XX PA (LEVA/) LEVANON A.

XX PI Lazarovits J, Nimrod A, Hoch MH, Levanon A;

XX WPI; 2004-746943/73.

XX Composition useful for treating diseases e.g., inflammatory diseases,

PT thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or

PT retinopathic diseases, comprises agent and antibody or its fragment.

XX Claim 13; SEQ ID NO 3; 22pp; English.

XX The invention relates to a composition which comprises an agent and an

CC antibody or its fragment. The composition is useful for inhibiting cell

CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,

CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet

CC and/or cell-platelet complex formation, aggregation or adhesion, increase

CC in number of tumour cells or growth and/or replication of tumour or

CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia

CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-

CC cancer agents, for decreasing number of tumour or leukaemia cells, or for

CC ameliorating the effect of a disease, preventing a disease, treating a

CC disease, or inhibiting the progress of a disease. The composition is

CC useful for therapeutic treatment, where antibody or its fragment and the

CC agent are administered separately. The antibody or its fragment is

CC administered prior to or subsequent to the agent. The composition is

CC useful for treating diseases such as inflammatory diseases, diseases

CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,

CC diseases involving abnormal or pathogenic aggregation, autoimmune

CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused

CC by sulphated tyrosine-dependent protein-protein interactions or diseased

CC cells. The present sequence represents the human leukaemia cell binding

CC scFv antibody fragment L32.

XX Sequence 280 AA;

XX Query Match 96.3%; Score 1386.5; DB 8; Length 280;

XX Best Local Similarity 96.8%; Pred. No. 2.1e-85;

Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAAQPAEAQVQVVGSGGVVRRPGGSLRLSCAASGFTFD---DYGMS 57

Db 1 MKYLLPTAAAGLLLLAAQPAEAQVQVVGSGGVVRRPGGSLRLSCAASGFTFDLNPVKYKM 60

QY 58 WYRQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRADETAVYY 117

Db 61 WYRQAPKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRADETAVYY 120

QY 118 CARMRAPVIWGQTLTVTSRGG 177

Db 121 CARMRAPVIWGQTLTVTSRGG 180

QY 178 LRSYASWYQKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237

Db 181 LRSYASWYQKPGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240

QY 238 CNSRDSSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277

Db 241 CNSRDSSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 280

RESULT 15

ADX01181

ID ADX01181 standard; protein; 280 AA.

XX AC ADX01181;

XX DT 21-APR-2005 (first entry)

XX Amino acid sequence for scFv antibody, SEQ ID No:56.

XX antibody; cancer; diagnosis; tumor; HIV infection; autoimmune disease;

KW metastasis; leukemia; platelet; antiaggregant; restenosis;

KW antibody dependent cell-mediated cytotoxicity; apoptosis;

KW natural killer cell; T-lymphocyte; inflammation; cardiovascular disease;

KW retinopathy; anti-HIV; cytostatic; immunosuppressive; antiinflammatory;

KW cardiovascular-gen.; ophthalmological; scFv.

XX Unidentified.

XX WO2005010153-A2.

XX PD 03-FEB-2005.

XX 30-JUN-2004; 2004WO-US021002.

XX 30-JUN-2003; 2003US-00611238.

XX (SAVI-) SAVIENT PHARM INC.

XX Plaksain D, Levanon A, Szanton E, Hagay Y, Ben-Levy R, Nisgav Y;

XX Szrajber T, Kanfi Y,

XX WPI; 2005-132536/14.

XX Novel antibody e.g., S15 antibody or their fragments useful for purging

PT tumor cells from patient or for treating autoimmune diseases,

PT inflammatory diseases, cardiovascular diseases or retinopathic diseases.

XX Claim 14; SEQ ID NO 56; 134pp; English.

XX The invention relates to antibodies e.g. S15 antibody, or their fragments

CC that bind to cancer cells. The antibodies or their fragments comprise a

CC consensus sequence (given as SEQ ID No:3 in the specification) of X1-X2-

CC X3-Pro-X5-X6, where X1 and X6 are hydrophobic amino acids and X2, X3 and

CC X5 are any amino acid. Also described are (i) a composition comprising

CC the antibody and a carrier, (ii) a diagnostic, prognostic or staging kit

CC comprising the antibody and an imaging agent, (iii) an isolated or

CC purified DNA sequence encoding the antibody, (iv) an expression vector

CC comprising the DNA sequence, (v) a recombinant host cell comprising the

CC expression vector, (vi) a method of producing the antibody, (vii) a

polypeptide comprising the consensus sequence, (viii) a method of selecting an antibody or their fragments or a polypeptide, (ix) an antibody or their fragment produced by the method, (x) a library of immunoglobulin binding domains, (xi) a small inorganic molecule that binds to a sulfated epitope of PSGL-1, GP1b and/or CCR5, and (xii) a composition comprising a small inorganic molecule. The antibody of the invention is useful for diagnosing, prognosing, or staging a disease in a patient which involves providing a sample containing a cell from the patient and determining whether the antibody binds to the cell of the patient, thus indicating that the patient is at risk or has the disease. The antibody is useful for purging tumor cells from a patient which involves providing a sample containing cells from the patient, and incubating the cells from the patient with the antibody, where purging occurs under ex vivo conditions. A composition comprising the antibody is useful for treating a disease (e.g. infection caused by HIV) or cell rolling, inhibiting autoimmune disease, metastasis or growth and/or replication of tumor or leukemic cells e.g. B-CLL cells, increasing the mortality rate of tumor or leukemic cells, altering the susceptibility of disease cells to damage by anti-disease agents, increasing the susceptibility of tumor or leukemic cells to damage by anticancer or antileukemic agents, inhibiting platelet aggregation or restenosis, eliciting antibody dependent cell-mediated cytotoxicity (ADCC), eliciting apoptosis in leukemic cells, or stimulating a natural killer (NK) cell or a T cell. ADCC is mediated by effector cells e.g. natural killer or monocytic cells. The composition is also useful for producing medicament useful for selecting a sulfated epitope that binds to the antigen-binding domain. The antibody is useful for treating cancer, leukemia, autoimmune diseases, inflammatory diseases, HIV infection, cardiovascular diseases, and retinopathic diseases. This sequence represents a scFv antibody.

XX Sequence 280 AA;

Qy	1	MKYLPTAAAGLLLLAAQPAVAEVLVESGGGVVPRPGSLRLSCAASGFTPD---	DYGMS	57
Db	1	MKYLPTAAAGLLLLAAQPAVAEVLVESGGGVVPRPGSLRLSCAASGFTPD---	LNPKVHM	60
Qy	58	WVROAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYLQWNSLR	AEDTAVYY	117
Db	61	WVROAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYLQWNSLR	AEDTAVYY	120
Qy	118	CARMRAPIVINGQGTAVTVSRGGSGGGSGGSSSELTQDPVAVSVALGQT	VRITCGDS	177
Db	121	CARLVRPFLMGQGTAVTVSRGGSGGGSGGSSSELTQDPVAVSVALGQT	VRITCGDS	180
Qy	178	LSRYASWYQKPGQAPVLIYIGNKRPSTGIPDRFSGSSSGNTASLTITGAQ	ADEADYY	237
Db	181	LSRYASWYQKPGQAPVLIYIGNKRPSTGIPDRFSGSSSGNTASLTITGAQ	ADEADYY	240
Qy	238	CNSRDSSGNHVFGGGTKLTVLGAABQKLI	SEEDLNAA	277
Db	241	CNSRDSSGNHVFGGGTKLTVLGAABQKLI	SEEDLNAA	280

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OM protein - protein search, using sw model

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(without alignments)
602.487 Million cell updates/sec

Title: US-10-029-926D-25
Perfect score: 1440
Sequence: 1 MKYLLPTAAAGLLLLAAQA.....VLGAAAEQKLISEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1278.5	88.8	280	2	US-09-260-527-1
2	1275.5	88.6	309	2	US-09-079-029-9
3	1194	82.9	312	2	US-09-079-029-10
4	1126.5	78.2	278	2	US-09-260-527-3
5	973	67.6	310	2	US-09-079-029-11
6	961.5	66.8	288	2	US-09-818-247-22
7	836.5	58.1	284	2	US-08-564-164A-2
8	829	57.6	282	1	US-08-860-174A-10
9	822	57.1	268	2	US-09-976-118-1
10	803	55.8	240	2	US-09-132-854-2
11	803	55.8	240	2	US-09-511-939-2
12	800	55.6	289	2	US-09-184-658-63
13	800	55.6	289	2	US-09-504-2620-63
14	797.5	55.4	334	2	US-09-646-028-53
15	797.5	55.4	339	2	US-09-646-028-55
16	791.5	55.0	348	2	US-09-646-028-51
17	787.5	54.7	245	2	US-08-918-148-75
18	787.5	54.7	245	2	US-09-138-091A-73
19	786.5	54.6	245	2	US-08-918-148-76
20	786.5	54.6	245	2	US-09-138-091A-74
21	786	54.6	255	2	US-09-553-498-8
22	786	54.6	255	2	US-09-618-869-8
23	781.5	54.3	245	2	US-08-918-148-78
24	781.5	54.3	245	2	US-09-138-091A-76
25	775	53.8	272	2	US-09-726-219A-183
26	775	53.8	272	2	US-09-196-522-183
27	772.5	53.6	301	1	US-08-661-052-14

Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 178, App
Sequence 178, App
Sequence 178, App
Sequence 178, App
Sequence 38, Appl
Sequence 77, Appl
Sequence 75, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 44, Appl
Sequence 7, Appl
Sequence 5, Appl
Sequence 78, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-260-527-1

; Sequence 1, Application US/09260527A

; Patent No. 6228599

; GENERAL INFORMATION:

; APPLICANT: Knox, J.P.

; APPLICANT: Mikkelson, J.D.

; APPLICANT: Willats, W. G.

; TITLE OF INVENTION: ANTIBODY

; FILE REFERENCE: DY0U19.001AUS

; CURRENT APPLICATION NUMBER: US/09/260,527A

; CURRENT FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 280

; TYPE: PRT

; ORGANISM: UNKNOWN

; FEATURE:

; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a

; OTHER INFORMATION: phage display library known as the Synthetic scFv

; OTHER INFORMATION: Library (#1) from the Centre for Protein

; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.

US-09-260-527-1

Query Match 88.8%; Score 1278.5; DB 2; Length 280;

Best Local Similarity 90.0%; Pred. No. 5.7e-96;

Matches 252; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

Qy 1 MKYLLPTAAAGLLLLAAQAQAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMWSVR 60

Db 1 MKYLLPTAAAGLLLLAAQAQAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMWSVR 60

Qy 61 QAPKGLEWVSGI--NWNGSGTGYADSVKGRFTISRDNAKNSLYLQNNSLRAEDTAVYVC 118

Db 61 QAPKGLEWVSGI--NWNGSGTGYADSVKGRFTISRDNAKNSLYLQNNSLRAEDTAVYVC 120

Qy 119 AR-MRAPVINGQGTTLVTVSRGG 177

Db 119 AR-MRAPVINGQGTTLVTVSRGG 180

Qy 178 LRSYASWYQKQGPAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 237

Db 181 LRSYASWYQKQGPAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYY 240

Qy 238 CNSRDSGNHVFVGKGTTLVGLGAAAEQKLISEDLNGAA 277

Db 241 CNSRDSGNHVFVGKGTTLVGLGAAAEQKLISEDLNGAA 280

RESULT 2

US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-9

Query Match 88.6%; Score 1275.5; DB 2; Length 309;
Best Local Similarity 89.9%; Pred. No. 1.1e-95;
Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

Qy 16 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTFDYGMVWVRQAPGKLEWVSGINW 75
Db 33 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTFDYGMVWVRQAPGKLEWVSGINW 92

Qy 76 NGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYYCARMRAP-----VIWQQ 129
Db 93 NGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYYCAKILGAGRMGYFDLWGK 152

Qy 130 GTLVTSRGG 189
Db 153 GTLVTSRGG 212

Qy 190 PQQAPVLVIYKGNRPFGIPDRFSGSSSGNTASLTITGAQAEADYTCNRSRDSGNHVV 249
Db 213 PQQAPVLVIYKGNRPFGIPDRFSGSSSGNTASLTITGAQAEADYTCNRSRDSGNHVV 272

Qy 250 FGGTGTTLVGLA-----AAEQKLISEEDLNGAA 277
Db 273 FGGTGTTLVGLAHHHHAABQKLISEEDLNGAA 309

RESULT 3

US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-10

Query Match 82.9%; Score 1194; DB 2; Length 312;
Best Local Similarity 85.0%; Pred. No. 4.6e-89;
Matches 238; Conservative 5; Mismatches 19; Indels 18; Gaps 2;

Qy 16 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTFDYGMVWVRQAPGKLEWVSGINW 75
Db 33 AAQPMALVQLVSGGGVVRPGGSLRLSCAASGFTFDYGMVWVRQAPGKLEWVSGINW 92

Qy 76 NGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYYCARMRAPV-----I 126
Db 93 DSGEKTYYDSVKGRTISRDNKNSLYLQNSLRAEDTAVYYCARDLLKYKSSSGWFDP 152

Qy 127 WGGTTLVTSRGG 186
Db 153 WGGTTLVTSRGG 212

Qy 187 QKPGQAPVLVIYKGNRPFGIPDRFSGSSSGNTASLTITGAQAEADYTCNRSRDSGN 246
Db 213 QKPGQAPVLVIYKGNRPFGIPDRFSGSSSGNTASLTITGAQAEADYTCNRSRDSGN 272

Qy 247 HVVFGGTTKLTVLGA-----AAEQKLISEEDLNGAA 277
Db 273 HVVFGGTTKLTVLGAHHHHAABQKLISEEDLNGAA 312

RESULT 4

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelsen, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3
LENGTH: 278
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected from a naive phage display library known as the
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match 78.2%; Score 1126.5; DB 2; Length 278;
Best Local Similarity 80.3%; Pred. No. 1.2e-83;
Matches 224; Conservative 17; Mismatches 35; Indels 3; Gaps 3;

Qy 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVSGGVVPRPGSLRLSCAASGFTDDYGVMSWV 59
Db 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVSGGVVPRPGSLRLSCAASGFTDDYGVMSWV 60

Qy 60 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCA 119
Db 61 QPPEKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCA 119

Qy 120 RMRAPVIVGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 178
Db 120 RMRAPVIVGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179

Qy 179 RSYVASWYQKPGQAPVLIYKKNRPSGIPDRFSGSSGNTASITITGAQAEDEADYYC 238
Db 180 RSYVASWYQKPGQAPVLIYKKNRPSGIPDRFSGSSGNTASITITGAQAEDEADYYC 239

Qy 239 NSRDSGHHVFGGTTKLTVLGAAAEQKLISEEDLNGAA 277
Db 240 NSRDSGHHVFGGTTKLTVLGAAAEQKLISEEDLNGAA 278

RESULT 5

US-09-079-029-11
Sequence 11, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chundharapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids

TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11

Query Match 67.6%; Score 973; DB 2; Length 310;
Best Local Similarity 71.9%; Pred. No. 3.7e-71;
Matches 200; Conservative 19; Mismatches 43; Indels 16; Gaps 4;

Qy 16 AAQAPMAEVQLVSGGVVPRPGSLRLSCAASGFTDDYGVMSWVROAPGKLEWVSGINW 75
Db 33 AAQAPMAEVQLVSGGVVPRPGSLRLSCAASGFTDDYGVMSWVROAPGKLEWVSGINW 92

Qy 76 NGSSTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPV---IWQGTGL 132
Db 93 DGGNKYYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPV---IWQGTGL 152

Qy 133 VTVSRGG 188
Db 153 VTVSRGG 212

Qy 189 KPGQAPVLIYKKNRPSGIPDRFSGSSGNTASITITGAQAEDEADYYCNSRDSGHHV 248
Db 213 LPTGAPKLLIYDSSNRPSGIPDRFSGSSGNTASITITGAQAEDEADYYCNSRDSGHHV 272

Qy 249 VFGGTTKLTVLGA-----AAEQKLISEEDLNGAA 277
Db 273 VFGGTTKLTVLGA-----AAEQKLISEEDLNGAA 310

RESULT 6

US-09-818-247-22
Sequence 22, Application US/09818247
Patent No. 6855810
GENERAL INFORMATION:
APPLICANT: Mostov, Keith E.
APPLICANT: Chapin, Steven J.
APPLICANT: Richman-Eisenstat, Janice
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. 6855810-Secretory Component,
TITLE OF INVENTION: No. 6855810-Stalk Region of p19R and Methods of Use Thereof
FILE REFERENCE: 18062E-000910US
CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 288
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence: Pelb/4AF/myc/6HIS
US-09-818-247-22

Query Match 66.8%; Score 961.5; DB 2; Length 288;
Best Local Similarity 69.4%; Pred. No. 2.9e-70;
Matches 197; Conservative 26; Mismatches 52; Indels 9; Gaps 4;

Qy 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVSGGVVPRPGSLRLSCAASGFTDDYGVMSWVR 60
Db 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVSGGVVPRPGSLRLSCAASGFTDDYGVMSWVR 60

Qy 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
Db 61 QAPGKLEWVSAISGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120

Qy 121 MRAP-----VWVGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 173

Db 241 VQAEGLAVYC--QNDYTYPTFGGKLEI---KREQKISEEDLN 282
||||| ||| ||| :: ||||| : ||||| |||||

RESULT 9
US-09-976-118-1
; Sequence 1, Application US/09976118
; Patent No. 669473
; GENERAL INFORMATION:
; APPLICANT: Raiesch, Kevin Paul
; APPLICANT: Curiel, David T.
; APPLICANT: Bonner, James Allen
; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Single-Chain Antibodies
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 268
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURES:
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFV
; OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

Query Match 57.1%; Score 822; DB 2; Length 268;
Best Local Similarity 67.3%; Pred. No. 5.4e-59;
Matches 169; Conservative 21; Mismatches 47; Indels 14; Gaps 3;
Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDYGMSWVRQAPGKGLVWSGGINMNGSGTGY 82
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLVWSAISNGSGTYY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV-----IWGGTGLV 133
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV-----IWGGTGLV 120
Qy 134 TVSRGGGGS-----GGGSGGGGSELQDPAPVVALGQTVRITCGDLSRSYASWYQOK 189
Db 121 TVSSGSASAPKLEGEFSEARVQSVLTQPPSLVSPGQTASITCGDKLGDKYASWYQOK 180
Qy 190 PGQAPLVIVYKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVV 249
Db 181 PGQSPVLIVYQDKRPSGIPDRFSGSSGNTATITISGTAQAEADYYCQAWDSSTPY-V 239
Qy 250 FGGGTGLTVLG 260
Db 240 FGTGTGLTVLG 250

RESULT 10
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-192-854-2
Query Match 55.8%; Score 803; DB 2; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.6e-57;
Matches 159; Conservative 27; Mismatches 48; Indels 6; Gaps 4;
Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDYGMSWVRQAPGKGLVWSGGINMNGSGTGY 82
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLVWSAISGGSTYY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV--IWGGTGLTVTSRGGG 141
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCAKYGAFDYWGQGLTVTVSSGGG 120
Qy 142 SGGGSGGGGSS--ELTQDP-AVSVALGQTVRITCGDLSRSYASWYQOKPGAPVLVI 198
Db 121 SGGGSGGGGSDIQTQSPSSLSASVGDRTVITCRASQSISLYLNWYQKPGKAPKLLI 180
Qy 199 YGKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLT 258
Db 181 YAASSLQSGVPSRPSGSGSGTDFLTITSSLPQDFATYYCQSYSTPN--TFGGGTKEI 238

RESULT 11
US-09-511-939-2
; Sequence 2, Application US/09511939
; Patent No. 6846634
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1070
; CURRENT APPLICATION NUMBER: US/09/511,939
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-511-939-2

Query Match 55.8%; Score 803; DB 2; Length 240;
Best Local Similarity 66.2%; Pred. No. 1.6e-57;
Matches 159; Conservative 27; Mismatches 48; Indels 6; Gaps 4;
Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDYGMSWVRQAPGKGLVWSGGINMNGSGTGY 82
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLVWSAISGGSTYY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCARMRAPV--IWGGTGLTVTSRGGG 141
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVTYCAKYGAFDYWGQGLTVTVSSGGG 120
Qy 142 SGGGSGGGGSS--ELTQDP-AVSVALGQTVRITCGDLSRSYASWYQOKPGAPVLVI 198
Db 121 SGGGSGGGGSDIQTQSPSSLSASVGDRTVITCRASQSISLYLNWYQKPGKAPKLLI 180
Qy 199 YGKNNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLT 258
Db 181 YAASSLQSGVPSRPSGSGSGTDFLTITSSLPQDFATYYCQSYSTPN--TFGGGTKEI 238

RESULT 12
US-09-184-658-63

```
; Sequence 63, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Otterness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
; OTHER INFORMATION: scFv.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: pCANTAB6 signal peptide; Val at position 1 is most
; OTHER INFORMATION: likely initiator Met.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (23)..(138)
; OTHER INFORMATION: 5109 VH domain.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (139)..(154)
; OTHER INFORMATION: 16 amino acid linker.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (155)..(266)
; OTHER INFORMATION: 5109 VL domain.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (270)..(279)
; OTHER INFORMATION: myc tag.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (284)..(289)
; OTHER INFORMATION: His tag.
; US-09-184-658-63

Query Match          55.6%; Score 800; DB 2; Length 289;
Best Local Similarity 60.3%; Pred. No. 3.6e-57;
Matches 175; Conservative 28; Mismatches 67; Indels 20; Gaps 8;

Qy      1 MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMWVR 60
Db      1 MKKLLFAIPLVPPFYAAQPAWAEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMWVR 60

Qy      61 QAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAR 120
Db      61 QTPDKRLWVATINSNGLTFYADSVKGRFTISRDNKNTLYLQNNRLKSGDSGMYYCVR 120

Qy      121 MRAPVI-WGGTGLTVTSRGGSGGGGGGGSSSE--LTQDP-AVSVALGQTVRITCQ-- 174
Db      121 GYSNYARWGGALVTYSSGGSGGGGGGGSDVVMTQTPLTSLVITIGQSASISCKSS 180

Qy      175 -----GDSLRSYASWYQKPGQAPVLIYVIGNKRRPSGIPDRPSGSSSGNTASITITGAQ 229
Db      181 QSLLGSDGLT--YLIWLLRPGQSPKRLIFLVSELDGVPDRFTGSGSGDFTLKISRAE 238

Qy      230 AEDBADYCNRSRDSGNHV--VFGGGTKLTVLGAABQKLISEEDLNAA 277
Db      239 AEDLGVIYC-----CQGHFPHFTGAGTKLE-LKAAAEQKLISEEDLNAA 283
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RESULT 13
US-09-504-262D-63
; Sequence 63, Application US/09504262D
; Patent No. 6642007
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Saltarelli, Mary J.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Otterness, Ivan G.
; TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
; FILE REFERENCE: PC10189GPR - CIP of PC9946A
; CURRENT APPLICATION NUMBER: US/09/504,262D
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5109 scFv from clone p5109C scFv7
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL scFv.
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: pCANTAB6 signal peptide; Val at position 1 is most likely initiat
; OTHER INFORMATION: Or Met.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (23)..(138)
; OTHER INFORMATION: 5109 VH domain.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (139)..(154)
; OTHER INFORMATION: 16 amino acid linker.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (155)..(266)
; OTHER INFORMATION: 5109 VL domain.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (270)..(279)
; OTHER INFORMATION: myc tag.
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (284)..(289)
; OTHER INFORMATION: His tag.
; US-09-504-262D-63
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Query Match          55.6%; Score 800; DB 2; Length 289;
Best Local Similarity 60.3%; Pred. No. 3.6e-57;
Matches 175; Conservative 28; Mismatches 67; Indels 20; Gaps 8;

Qy      1 MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMWVR 60
Db      1 MKKLLFAIPLVPPFYAAQPAWAEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMWVR 60

Qy      61 QAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQNNLSRAEDTAVYYCAR 120
Db      61 QTPDKRLWVATINSNGLTFYADSVKGRFTISRDNKNTLYLQNNRLKSGDSGMYYCVR 120

Qy      121 MRAPVI-WGGTGLTVTSRGGSGGGGGGGSSSE--LTQDP-AVSVALGQTVRITCQ-- 174
Db      121 GYSNYARWGGALVTYSSGGSGGGGGGGSDVVMTQTPLTSLVITIGQSASISCKSS 180

Qy      175 -----GDSLRSYASWYQKPGQAPVLIYVIGNKRRPSGIPDRPSGSSSGNTASITITGAQ 229
Db      181 QSLLGSDGLT--YLIWLLRPGQSPKRLIFLVSELDGVPDRFTGSGSGDFTLKISRAE 238
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Result No.	Query			ID	Description	
	Score	Match	Length			
1	1440	100.0	277	15	US-10-032-037B-25	Sequence 25, Appl
2	1440	100.0	277	15	US-10-029-988B-25	Sequence 25, Appl
3	1440	100.0	277	15	US-10-032-423A-25	Sequence 25, Appl
4	1440	100.0	277	15	US-10-029-926B-25	Sequence 25, Appl
5	1416	98.3	277	15	US-10-032-037B-203	Sequence 203, App
6	1416	98.3	277	15	US-10-029-988B-203	Sequence 203, App
7	1416	98.3	277	15	US-10-032-423A-203	Sequence 203, App
8	1416	98.3	277	15	US-10-029-926B-203	Sequence 203, App
9	1388.5	96.4	280	17	US-10-880-922-6	Sequence 6, Appli
10	1379.5	95.8	280	17	US-10-880-922-5	Sequence 5, Appli
11	1379.5	95.8	280	17	US-10-880-922-56	Sequence 56, Appl
12	1378.5	95.7	280	17	US-10-880-922-60	Sequence 60, Appl
13	1378	95.7	266	15	US-10-032-037B-204	Sequence 204, App

RESULT 5
US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Qy 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Qy 121 MRAPVINGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Db 121 MRAPVINGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Qy 121 LTHPYFVGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Db 121 LTHPYFVGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Qy 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLITITGAQAEDEADYYCNS 240
Db 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLITITGAQAEDEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277
Db 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277

RESULT 6
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60

Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Qy 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Qy 121 MRAPVINGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Db 121 MRAPVINGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Qy 121 LTHPYFVGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Db 121 LTHPYFVGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Qy 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLITITGAQAEDEADYYCNS 240
Db 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLITITGAQAEDEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277
Db 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277

RESULT 7
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGVVRPGGSLRLSCAASGFTFDDYGMWVR 60
Qy 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCAR 120
Qy 121 MRAPVINGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Db 121 MRAPVINGQGLTVTVSRGGSGGGGGSSSLTQDPAVSVALGQTVRITCGDLSLR 180
Qy 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLITITGAQAEDEADYYCNS 240
Db 181 YYASWYQKPGQAPVLIYGNKRRPSGIPDRFSGSSSGNTASLITITGAQAEDEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277
Db 241 RDSSGNHVFGGKTLTVLGAARAEQKLISEEDLNGAA 277

RESULT 8
US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040007301A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY

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; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-203

Query Match      98.3%; Score 1416; DB 15; Length 277;
Best Local Similarity 98.2%; Pred. No. 2.6e-86;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVR 60
   |||||
Db 1 MKYLLPTAAAGLLLLAAQPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVR 60
   |||||

Qy 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
   |||||
Db 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
   |||||

Qy 121 MRAPVINGQGTLTVTVRSGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDSLRS 180
   |||||
Db 121 LTHFYFGQGTTLVTVRSGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDSLRS 180
   |||||

Qy 181 YYASWYQKPGQAPLVLYYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
   |||||
Db 181 YYASWYQKPGQAPLVLYYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240
   |||||

Qy 241 RDSGNGHVFGGGTKLTVLGAABQKLISEEDLNGAA 277
   |||||
Db 241 RDSGNGHVFGGGTKLTVLGAABQKLISEEDLNGAA 277
   |||||

RESULT 9
US-10-880-922-6
; Sequence 6, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YAEEL
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensus antibody
US-10-880-922-6

Query Match      95.8%; Score 1379.5; DB 17; Length 280;
Best Local Similarity 96.1%; Pred. No. 7.7e-86;
Matches 269; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

Qy 1 MKYLLPTAAAGLLLLAAQPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMW 57
   |||||
Db 1 MKYLLPTAAAGLLLLAAQPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDLNPVKHM 60
   |||||

Qy 58 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 117
   |||||
Db 58 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 117
   |||||

Qy 61 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 120
   |||||
Db 61 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 120
   |||||

Qy 118 CARMRAPVINGQGTLTVTVRSGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDS 177
   |||||
Db 118 CARMRAPVINGQGTLTVTVRSGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDS 177
   |||||

Qy 121 CARMRAPVINGQGTLTVTVRSGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDS 180
   |||||
Db 121 CARMRAPVINGQGTLTVTVRSGGGGGGGGGSSSELTDQPAVSVALGQTVRITCGDS 180
   |||||

Qy 178 LRSYASWYQKPGQAPLVLYYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
   |||||
Db 178 LRSYASWYQKPGQAPLVLYYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
   |||||

Qy 181 LRSYASWYQKPGQAPLVLYYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
   |||||
Db 181 LRSYASWYQKPGQAPLVLYYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
   |||||

Qy 238 CNSRDSGNGHVFGGGTKLTVLGAABQKLISEEDLNGAA 277
   |||||
Db 238 CNSRDSGNGHVFGGGTKLTVLGAABQKLISEEDLNGAA 277
   |||||

Qy 241 CNSRDSGNGHVFGGGTKLTVLGAABQKLISEEDLNGAA 280
   |||||
Db 241 CNSRDSGNGHVFGGGTKLTVLGAABQKLISEEDLNGAA 280
   |||||

RESULT 10
US-10-880-922-5
; Sequence 5, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YAEEL
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensus antibody
US-10-880-922-5

Query Match      96.4%; Score 1388.5; DB 17; Length 280;
Best Local Similarity 96.8%; Pred. No. 1.9e-86;
Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

Qy 1 MKYLLPTAAAGLLLLAAQPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMW 57
   |||||
Db 1 MKYLLPTAAAGLLLLAAQPAMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMW 57
   |||||
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RESULT 11

US-10-880-922-56
; Sequence 56, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YABL
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensu antibody
US-10-880-922-56

Query Match 95.8%; Score 1379.5; DB 17; Length 280;
Best Local Similarity 95.7%; Pred. No. 7.7e-86;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDL	57
Db	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDL	60
Qy	58	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVY	117
Db	61	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVY	120
Qy	118	CARMAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	177
Db	121	CARLRPFLWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	180
Qy	178	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAE	237
Db	181	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAE	240
Qy	238	CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA	277
Db	241	CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA	280

RESULT 12

US-10-880-922-60
; Sequence 60, Application US/10880922
; Publication No. US20050069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, YABL
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 60
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensu antibody
US-10-880-922-60

Query Match 95.7%; Score 1378.5; DB 17; Length 280;
Best Local Similarity 95.7%; Pred. No. 9e-86;
Matches 268; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

Qy	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDL	57
Db	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDL	60
Qy	58	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVY	117
Db	61	WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVY	120
Qy	118	CARMAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	177
Db	121	CARLRPFLWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDS	180
Qy	178	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAE	237
Db	181	LRSYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAE	240
Qy	238	CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA	277
Db	241	CNSRDSGNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA	280

RESULT 13

US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDL	60
Db	1	MKYLLPTAAAGLLLLAAQPAWAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDL	60
Qy	61	QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVY	120
Db	61	QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMSLRAEDTAVY	120
Qy	121	MRAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDSL	180
Db	121	MRAPVWGQGLTVTVSRGGSGGGGGSSSELTDPAVSVVALGQTVRITCGDSL	180
Qy	181	YASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAE	240

Db 181 YYASWYQKPGQAPVLVIYGNRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Qy 241 RDSSGNHVFGGKTLVLGAAABQK 266
Db 241 RDSSGNHVFGGKTLVLGAAAKAK 266

RESULT 14
US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60

Qy 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

Qy 121 MRAPVWGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVVALGQTVRITCGDSLRS 180
Db 121 MRAPVWGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVVALGQTVRITCGDSLRS 180

Qy 181 YYASWYQKPGQAPVLVIYGNRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Db 181 YYASWYQKPGQAPVLVIYGNRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240

Qy 241 RDSSGNHVFGGKTLVLGAAABQK 266
Db 241 RDSSGNHVFGGKTLVLGAAAKAK 266

RESULT 15
US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-032-423A-204

Query Match 95.7%; Score 1378; DB 15; Length 266;
Best Local Similarity 99.2%; Pred. No. 9.3e-86;
Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60
Db 1 MKYLLPTAAAGLLLLAAQAPMAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMWVR 60

Qy 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
Db 61 QAPKGLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

Qy 121 MRAPVWGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVVALGQTVRITCGDSLRS 180
Db 121 MRAPVWGQGLTVTVSRGGGGGGGGSSSLTQDPAVSVVALGQTVRITCGDSLRS 180

Qy 181 YYASWYQKPGQAPVLVIYGNRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Db 181 YYASWYQKPGQAPVLVIYGNRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240

Qy 241 RDSSGNHVFGGKTLVLGAAABQK 266
Db 241 RDSSGNHVFGGKTLVLGAAAKAK 266

Search completed: April 25, 2005, 21:09:47
Job time : 122.531 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:47:37 ; Search time 123.208 Seconds
(without alignments)
939.375 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKYLLPTAAAGLLLLAAQPA.....VLGAAAEQKLISEEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1440	100.0	277	4	US-10-032-037B-25
2	1440	100.0	277	4	US-10-029-988B-25
3	1440	100.0	277	4	US-10-032-423A-25
4	1440	100.0	277	4	US-10-029-926B-25
5	1436	99.7	277	4	US-10-610-843B-1
6	1416	98.3	277	4	US-10-032-037B-203
7	1416	98.3	277	4	US-10-029-988B-203
8	1416	98.3	277	4	US-10-032-423A-203
9	1416	98.3	277	4	US-10-029-926B-203
10	1397.5	97.0	278	4	US-10-610-843B-2
11	1393.5	96.8	280	4	US-10-611-588C-1
12	1388.5	96.4	280	5	US-10-880-922-6
13	1386.5	96.3	280	4	US-10-610-843B-3
14	1379.5	95.8	280	5	US-10-880-922-5
15	1379.5	95.8	280	5	US-10-880-922-56
16	1378.5	95.7	280	5	US-10-880-922-60
17	1378	95.7	266	4	US-10-032-037B-204
18	1378	95.7	266	4	US-10-029-988B-204
19	1378	95.7	266	4	US-10-032-423A-204
20	1375.5	95.5	280	5	US-10-880-922-61
21	1374.5	95.5	280	5	US-10-880-922-55
22	1294	89.9	291	4	US-10-406-830-6
23	1275.5	88.6	309	4	US-10-052-798-9
24	1275.5	88.6	309	4	US-10-288-917-9
25	1275.5	88.6	309	4	US-10-423-448-9
26	1218.5	84.6	239	3	US-09-880-748-937
27	1218.5	84.6	239	4	US-10-293-418-937

28	1212.5	84.2	239	3	US-09-880-748-2038
29	1212.5	84.2	239	4	US-10-293-418-2038
30	1201.5	83.4	290	3	US-09-969-748C-2
31	1201.5	83.4	290	3	US-09-949-039-2
32	1201.5	83.4	290	5	US-10-470-987-42
33	1194	82.9	312	4	US-10-052-798-10
34	1194	82.9	312	4	US-10-288-917-10
35	1194	82.9	312	4	US-10-423-448-10
36	1191.5	82.7	239	3	US-09-880-748-2015
37	1191.5	82.7	239	4	US-10-293-418-2015
38	1188.5	82.5	296	3	US-09-969-748C-12
39	1188.5	82.5	296	3	US-09-949-039-75
40	1178	81.8	244	4	US-10-322-673-42
41	1178	81.8	244	5	US-10-981-465-42
42	1178	81.8	244	5	US-10-981-621-42
43	1178	81.8	244	5	US-10-981-673-42
44	1178	81.8	244	5	US-10-981-691-42
45	1149	79.8	242	6	US-11-017-030-28

ALIGNMENTS

RESULT 1

US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match 100.0%; Score 1440; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKYLPTAAAGLLLLAAQPA	MAEVQLV	ESGGVVR	PGGSLRL	SCAASGFT	DDYGM	SWVR	60			
Db	1	MKYLPTAAAGLLLLAAQPA	MAEVQLV	ESGGVVR	PGGSLRL	SCAASGFT	DDYGM	SWVR	60			
Qy	61	QAPGKLEWVSGINWNGSG	STGYADSV	KGRFTT	ISRDNA	KNLSYLQ	MNSLRA	EDTAV	YTCAR	120		
Db	61	QAPGKLEWVSGINWNGSG	STGYADSV	KGRFTT	ISRDNA	KNLSYLQ	MNSLRA	EDTAV	YTCAR	120		
Qy	121	MRAPVWQGTTLVTVSR	GGSGGGSG	GGSGG	SELTD	PAVSVAL	GTVTR	ITCGD	SLRS	180		
Db	121	MRAPVWQGTTLVTVSR	GGSGGGSG	GGSGG	SELTD	PAVSVAL	GTVTR	ITCGD	SLRS	180		
Qy	181	YYASWYQQKPGQAP	FLVLYG	KNRPSGI	PD	RFSSSG	SGNTAS	LTIT	CAQAE	DEADY	CNS	240
Db	181	YYASWYQQKPGQAP	FLVLYG	KNRPSGI	PD	RFSSSG	SGNTAS	LTIT	CAQAE	DEADY	CNS	240
Qy	241	RDSSGNHVP	GGTKLTV	LGA	AAEQK	LI	SEED	LNGAA	277			
Db	241	RDSSGNHVP	GGTKLTV	LGA	AAEQK	LI	SEED	LNGAA	277			

RESULT 2

US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 277

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-610-843B-1

Query Match 99.7%; Score 1436; DB 4; Length 277;

Best Local Similarity 99.6%; Pred. No. 1.5e-89;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPAWAEVQLVSGGVVPPGGSRLSCAASGFTFDDYGMWVR 60

DB 1 MKYLLPTAAAGLLLLAAQPAWAEVQLVSGGVVPPGGSRLSCAASGFTFDDYGMWVR 60

QY 61 QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

DB 61 QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

QY 121 MRAPVINGQGTLLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRS 180

DB 121 MRAPVINGQGTLLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRS 180

QY 181 YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

DB 181 YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

QY 241 RDSSGNHVVFGGTKLTVLGAAAEQKLISEEDLNGAA 277

DB 241 RDSSGNHVVFGGTKLTVLGAAAEQKLISEEDLNGAA 277

RESULT 6

US-10-032-037B-203

; Sequence 203, Application US/10032037B

; Publication No. US20040001822A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE OF INVENTION: MOETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/44

; CURRENT APPLICATION NUMBER: US/10/032,037B

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 203

; LENGTH: 277

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-037B-203

Query Match 98.3%; Score 1416; DB 4; Length 277;

Best Local Similarity 98.2%; Pred. No. 3.4e-88;

Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPAWAEVQLVSGGVVPPGGSRLSCAASGFTFDDYGMWVR 60

DB 1 MKYLLPTAAAGLLLLAAQPAWAEVQLVSGGVVPPGGSRLSCAASGFTFDDYGMWVR 60

QY 61 QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

DB 61 QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

QY 121 MRAPVINGQGTLLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRS 180

DB 121 LTHPYFWGQGTLLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRS 180

QY 181 YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

DB 181 YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

QY 241 RDSSGNHVVFGGTKLTVLGAAAEQKLISEEDLNGAA 277

DB 241 RDSSGNHVVFGGTKLTVLGAAAEQKLISEEDLNGAA 277

RESULT 7

US-10-029-988B-203

; Sequence 203, Application US/10029988B

; Publication No. US20040001839A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE OF INVENTION: MOETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/46

; CURRENT APPLICATION NUMBER: US/10/029,988B

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 203

; LENGTH: 277

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-029-988B-203

Query Match 98.1%; Score 1416; DB 4; Length 277;

Best Local Similarity 98.2%; Pred. No. 3.4e-88;

Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPAWAEVQLVSGGVVPPGGSRLSCAASGFTFDDYGMWVR 60

DB 1 MKYLLPTAAAGLLLLAAQPAWAEVQLVSGGVVPPGGSRLSCAASGFTFDDYGMWVR 60

QY 61 QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

DB 61 QAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120

QY 121 MRAPVINGQGTLLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRS 180

DB 121 LTHPYFWGQGTLLVTVSRGGSGGGGGSSSELTQDPAVSVALGQTVRITCGDSLRS 180

QY 181 YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

DB 181 YYASWYQKPGQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240

QY 241 RDSSGNHVVFGGTKLTVLGAAAEQKLISEEDLNGAA 277

DB 241 RDSSGNHVVFGGTKLTVLGAAAEQKLISEEDLNGAA 277

RESULT 8

US-10-032-423A-203

; Sequence 203, Application US/10032423A

; Publication No. US20040002450A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE OF INVENTION: MOETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/45

; CURRENT APPLICATION NUMBER: US/10/032,423A

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 203

; LENGTH: 277

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-423A-203

Query Match 98.3%; Score 1416; DB 4; Length 277;

```
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-610-843B-2

Query Match      98.2%; Score 1416; DB 4; Length 277;
Best Local Similarity 98.2%; Pred. No. 3.4e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWSVR 60
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWSVR 60
QY 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
Db 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
QY 121 MRAPVIMWGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Db 121 LTHPYFMGGGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 181 YYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Db 181 YYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
QY 241 RDSGNNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
Db 241 RDSGNNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
```

RESULT 9

```
US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-029-926B-203

Query Match      98.3%; Score 1416; DB 4; Length 277;
Best Local Similarity 98.2%; Pred. No. 3.4e-88;
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWSVR 60
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWSVR 60
QY 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
Db 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAR 120
QY 121 MRAPVIMWGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Db 121 LTHPYFMGGGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 181 YYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
Db 181 YYASWYQOKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNS 240
QY 241 RDSGNNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
Db 241 RDSGNNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
```

RESULT 10

```
US-10-610-843B-2
; Sequence 2, Application US/10610843B
; Publication No. US20040202665A1

Query Match      96.8%; Score 1393.5; DB 4; Length 280;
Best Local Similarity 97.1%; Pred. No. 1.1e-86;
Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWS 57
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWS 60
QY 58 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 117
Db 61 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 120
```

```
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-610-843B-2

Query Match      97.0%; Score 1397.5; DB 4; Length 278;
Best Local Similarity 97.8%; Pred. No. 6.1e-87;
Matches 272; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWSV 59
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWSV 60
QY 60 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCA 119
Db 61 QAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCA 120
QY 120 RMRAPVIMWGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 179
Db 121 RMRAPVIMWGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 180 SYVASWYQOKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCN 239
Db 181 SYVASWYQOKPGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYYCN 240
QY 240 SRDSSGNNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 277
Db 241 SRDSSGNNHVVFGGKTLTVLGAAAEQKLISEEDLNGAA 278
```

RESULT 11

```
US-10-611-588C-1
; Sequence 1, Application US/10611588C
; Publication No. US20040208877A1
; GENERAL INFORMATION:
; APPLICANT: Levanon, et al.
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793/70
; CURRENT APPLICATION NUMBER: US/10/611,588C
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,491
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-611-588C-1

Query Match      96.8%; Score 1393.5; DB 4; Length 280;
Best Local Similarity 97.1%; Pred. No. 1.1e-86;
Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWS 57
Db 1 MKYLLPTAAAGLLLLAAQPMARVQLVSGGGVVRPGGSLRLSCAASGFTFDDYGMWS 60
QY 58 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 117
Db 61 WVRQAPGKGLEWVSGINWNGSGTGADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYY 120
```


Db 1 MKYLLPTAAAGLLALLAAQPMABEVQVVGSGVVRPGSLRLSCAASGFTFDLNPVKHM 60
Qy 58 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNLSLYLQMSLRAEDTAVYY 117
Db 61 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNLSLYLQMSLRAEDTAVYY 120
Qy 118 CARMRAPIVWGQGLTVTVSRGGSGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDS 177
Db 121 CARLRPSIWGGGLTVTVSRGGSGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDS 180
Qy 178 LRSYASWYQKQKQAPVLIYGNKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
Db 181 LRSYASWYQKQKQAPVLIYGNKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
Qy 238 CNSRDSGNHVFVGGGKLTVLGAAAEQKLISEEDLNGAA 277
Db 241 CNSRDSGNHVFVGGGKLTVLGAAAEQKLISEEDLNGAA 280

RESULT 15

US-10-880-922-56
; Sequence 56, Application US/10880922
; Publication No. US2005069955A1
; GENERAL INFORMATION:
; APPLICANT: PLAKSIN, DANIEL
; APPLICANT: LEVANON, AVIGDOR
; APPLICANT: SZANTON, ESTHER
; APPLICANT: HAGAY, YOCHAVED
; APPLICANT: BEN-LEVY, RACHEL
; APPLICANT: NISGAV, Yael
; APPLICANT: KANFI, YARIV
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793-143
; CURRENT APPLICATION NUMBER: US/10/880,922
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/484,061
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 56
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Consensus antibody
US-10-880-922-56

Query Match 95.8%; Score 1379.5; DB 5; Length 280;
Best Local Similarity 95.7%; Pred. No. 1e-85; Mismatches 2; Indels 3; Gaps 1;
Matches 268; Conservative 7; Indels 3; Gaps 1;
Qy 1 MKYLLPTAAAGLLALLAAQPMABEVQVVGSGVVRPGSLRLSCAASGFTFDLNPVKHM 57
Db 1 MKYLLPTAAAGLLALLAAQPMABEVQVVGSGVVRPGSLRLSCAASGFTFDLNPVKHM 60
Qy 58 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNLSLYLQMSLRAEDTAVYY 117
Db 61 WVRQAPGKLEWVSGINWNGSGTGADSVKGRFTISRDNKNLSLYLQMSLRAEDTAVYY 120
Qy 118 CARMRAPIVWGQGLTVTVSRGGSGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDS 177
Db 121 CARLRPSIWGGGLTVTVSRGGSGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDS 180
Qy 178 LRSYASWYQKQKQAPVLIYGNKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 237
Db 181 LRSYASWYQKQKQAPVLIYGNKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY 240
Qy 238 CNSRDSGNHVFVGGGKLTVLGAAAEQKLISEEDLNGAA 277
Db 241 CNSRDSGNHVFVGGGKLTVLGAAAEQKLISEEDLNGAA 280

Search completed: November 18, 2005, 22:17:52
Job time : 124.208 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:53:49 ; Search time 3.49527 Seconds
(without alignments)
89.536 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKYLLPFAAGLLLLAQA.....VLGAABEQKLISEEDLNGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	719	49.9	625	1	US-10-512-184-47
2	690	47.9	269	1	US-10-839-799-109
3	676.5	47.0	618	1	US-10-512-184-48
4	672	46.7	250	1	US-10-512-184-27
5	672	46.7	327	1	US-10-512-184-62
6	672	46.7	327	1	US-10-512-184-64
7	672	46.7	328	1	US-10-512-184-63
8	672	46.7	576	1	US-10-512-184-65
9	670	46.5	252	1	US-10-512-184-28
10	668.5	46.4	313	1	US-10-512-184-72
11	649.5	45.1	329	1	US-10-512-184-68
12	648	45.0	258	1	US-10-512-184-26
13	644.5	44.8	261	1	US-10-512-184-35
14	641.5	44.5	263	1	US-10-512-184-29
15	638.5	44.3	329	1	US-10-512-184-70
16	629	43.7	320	1	US-10-512-184-67
17	629	43.7	569	1	US-10-512-184-66
18	625.5	43.4	259	1	US-10-512-184-31
19	614.5	42.7	251	1	US-10-512-184-33
20	605	42.0	259	1	US-10-512-184-30
21	604.5	42.0	626	1	US-10-512-184-49
22	604	41.9	543	1	US-10-495-664-3
23	573.5	39.8	317	1	US-10-512-184-69
24	557	38.7	371	1	US-10-512-184-71
25	553	38.4	615	1	US-10-512-184-50

26	549.5	38.2	248	1	US-10-512-184-32	Sequence 32, Appl
27	533	37.0	259	1	US-10-512-184-34	Sequence 34, Appl
28	490.5	34.1	444	7	US-11-172-320-6	Sequence 6, Appl
29	488.5	33.9	122	7	US-11-144-248-24	Sequence 24, Appl
30	485	33.7	470	7	US-11-144-248-46	Sequence 46, Appl
31	481.5	33.4	248	1	US-10-512-184-36	Sequence 36, Appl
32	480	33.3	138	1	US-10-789-273-8	Sequence 8, Appl
33	479.5	33.3	473	7	US-11-144-248-50	Sequence 50, Appl
34	478	33.2	121	1	US-10-789-273-9	Sequence 9, Appl
35	477	33.1	138	1	US-10-789-273-12	Sequence 12, Appl
36	474	32.9	470	7	US-11-144-248-49	Sequence 49, Appl
37	469	32.6	125	7	US-11-144-248-16	Sequence 16, Appl
38	468.5	32.5	139	1	US-10-721-763-33	Sequence 33, Appl
39	466	32.4	470	7	US-11-144-248-45	Sequence 45, Appl
40	451	31.3	124	7	US-11-144-248-8	Sequence 8, Appl
41	446	31.0	98	1	US-10-789-273-10	Sequence 10, Appl
42	446	31.0	98	7	US-11-144-248-32	Sequence 32, Appl
43	439	30.5	98	7	US-11-144-248-30	Sequence 30, Appl
44	423	29.4	121	7	US-11-077-978-2	Sequence 2, Appl
45	420.5	29.2	120	7	US-11-077-978-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-10-512-184-47
; Sequence 47, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFV CWP2 - cmvc/His6.
US-10-512-184-47

Query Match	49.9%	Score 719;	DB 1;	Length 625;
Best Local Similarity	57.2%	Pred. No. 2e+30;		
Matches 162;	Conservative 23;	Mismatches 68;	Indels 30;	Gaps 9;
Qy	16	AAQPMABVLSGSGGVVPPGGSLRLSCAASGFTPDYGMVSWVRQAPGKLEWVSGINW 75		
Db	337	AAQPMABVLSGSGGLQTPGGGLSLVCKSGDFSDTMMVVRQAPGKLEFVAGISG 396		
Qy	76	NGSGTGVADSVKGPFTISRDNKNSLYLQNSLRAEDTAVYICARMAPV----- 125		
Db	397	DGSDTNYGSAVKGRATISRDNQSGSTVRLQLNLRADTATYICT--RGPCSPTRKCAADR 454		
Qy	126	--TWGQGTTLTVSRGG--GGSGGGGGGG--GSSSELQDPAVSVALGOTVTRITCGDSL 179		
Db	455	IDAWGHTEVTIVSGSGTSGSGKPGPGGSGTKGAPALTPQSPVSNILGTVETICSGG--- 511		
Qy	180	SYASWYQOK-PCQAPVLVITYGN---NRPSGIPDRFSGSSSGNTASLITITGAQAEAD 235		
Db	512	GTRYGNFQOKSPGAPVTVIYWDSDSANRPSNIPSRFSGTSGSTATLTITGVQADDEAV 571		
Qy	236	YCNRRDSSGNHV-VFCGGTKLTVLG-----AAAEQKLISEDL 273		
Db	572	YFCGSDRRSGYVIFGAGTTLTVLGQFVDAAAEQKLISEDL 614		

```

RESULT 2
US-10-839-799-109
; Sequence 109, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-839-799-109

Query Match 47.9%; Score 690; DB 1; Length 269;
Best Local Similarity 53.8%; Pred. No. 3.1e-29;
Matches 142; Conservative 39; Mismatches 73; Indels 10; Gaps 5;

Qy 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWR 60
Db 1 MKYLLPTAAGLLLLAQAQMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWR 60
Qy 61 QAPGKGLWYSGINWNGSTCYADSVKGRFTISRDNAKNSLYLQNSLRARDETAVYICAR 120
Db 61 QAPGKGLWYSGINWNGSTCYADSVKGRFTISRDNAKNSLYLQNSLRARDETAVYICAR 120
Qy 121 MRAPVI---WGQGLTVTSRGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCO 174
Db 121 MRAPVI---WGQGLTVTSRGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCO 174
Qy 175 GDSLSRSYASNYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEAD 234
Db 175 GDSLSRSYASNYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEAD 234
Qy 179 ASQNVGTNVAWYQKPGKAPKPLIYASVYSGVPSRFGSGSGTDTFTTISLQPDIA 238
Db 179 ASQNVGTNVAWYQKPGKAPKPLIYASVYSGVPSRFGSGSGTDTFTTISLQPDIA 238
Qy 235 DYCNRSNDSGNHVVFQGGTKLTV 258
Db 235 DYCNRSNDSGNHVVFQGGTKLTV 258

RESULT 3
US-10-512-184-48
; Sequence 48, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFv VD2 - cmc/His6.
US-10-512-184-48

Query Match 47.0%; Score 676.5; DB 1; Length 618;
Best Local Similarity 52.7%; Pred. No. 2.4e-28;
Matches 145; Conservative 38; Mismatches 71; Indels 21; Gaps 8;

Qy 16 AAQPMAAEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWRQAPGKGLWVSGINW 75
Db 337 AAQPMAAEQVLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMSSWRQAPGKGLWVSGINW 396
Qy 76 NGSTGYADSVKGRFTISRDNAKNSLYLQNSLRARDETAVYICAR-MRAPV-----TWQGG 130
Db 397 YTGATYADSVKGRFTISRDNAKNSLYLQNSLRARDETAVYICAR-MRAPV-----TWQGG 456
Qy 131 TLVTSRGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCOG-----SLRSYIA 183
Db 457 TSVTSAAGGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRITCOG-----SLRSYIA 516
Qy 184 SWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNRSRDS 243
Db 517 QWYQKPGQAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNRSRDS 572
Qy 244 SGNHV--VFQGGTKLTV---LGRAAEQKLISEEDL 273
Db 573 QGSHVPTFGGTKLEIKRAVDAAEQKLISEEDL 607

RESULT 4
US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with

```

; OTHER INFORMATION: specificity against Pusarium ssp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match	46.7%	Score 672;	DB 1;	Length 250;
Best Local Similarity	58.2%	Fred. NO. 2.2e-28;		
Matches 146;	Conservative 24;	Mismatches 67;	Indels 14;	Gaps 6
Qy	21	MAEYOLVESGGGVVPPGSLRLSCAASGFTFDDYGMWSVVRQAPGKGLEWVSGINWNGGST	80	
Db	1	MAAVTLDESGGGLQTPGGALSIVCKASGFTFSSNGMAWVRQAPGKGLEWVAGIDGGSGFT	60	
Qy	81	GYADSVKGRFTISRDNAKNSLYLQNNSLRAREDYVYYCARMRPV-----IWGGTILVT	134	
Db	61	GYGAHVGRATISRDNGSTVRLQLNNLRAREDATYYICARTGGPGGDRIDAWHGHTVT	120	
Qy	135	VSRGG-GSGSGGSGGGG--GSELTQDPAYVSVALGTQVTRITCGQDSLRYSYASWYQOK-	189	
Db	121	VSSGSTSGSGKPGPGEGSTKCAPALTPQSSVSANLGGTVKITSCTSGST--AHY-SWHQQKS	177	
Qy	190	PGQAPVLVIYCKNNRPSGIPDRFSGSSSGNTASLTITCAQADEADYYCNSRDSGSHVV	249	
Db	178	PGSAPVTLISFNRRNPDPISRFPSGSKSGSTGLTITIGVRADEAVYYICGGWDRSITAGL	237	
Qy	250	FGGCTKLTVLG	260	
Db	238	FGAGTTLTTLVLG	248	

```

RESULT 5
US-10-512-184-62
; Sequence 62, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 327
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising AG - linker -
; OTHER INFORMATION: scFv CWPd2.
US-10-512-184-62

```

Query Match	46.7%	Score 672;	DB 1;	Length 327;
Best Local Similarity	56.0%;	Pred. No. 2.7e-28;		
Matches 149;	Conservative 23;	Mismatches 68;	Indels 26;	Gaps 8;
Qy	16	AAOPAAAEVOLVESGGGVPRGGSLRLSCAASGFTEDDYGMWSVYRQAPGKLEWVSGINW	75	
Db	65	AAOPAAAVTLDSEGGGLQTFGGGLSLVCKSGGDFSSDTMMWYRQAPGKLEFPVAGISG	124	
Qy	76	NGSGTGYADVSKGRFTTIRDNNAKNSLYLQNNLSLAEDTAVYYCARMAPV----	125	
Db	125	DGSDNTYGSVAKGRATISRDNGQSTVRLQLMNLRAEDTATYCT--RGPCSPTKNCAADR	182	
Qy	126	--TWGCGTTLTVSVRGG--GGSGGGSGGGG---GSSELQDPAVSVALCGTVRIITCGDSL	179	
Db	183	IDAWGHTETVSVSGSTSGSGKPGPGSGSTKGAPALIQPSVSNLGGTVEITCSGG---	239	
Qy	180	SYVASVTQOK--PGQAPVLVIYGRK---NRPSGIPDRFGSSSGNGTASLTITGAQAEAD	235	
Db	240	GYRGMFQOKSPGSAPTVTVYWDSDSANRSENTPSRFGSGTSGSTATLTITGVOADDEAV	299	

```

Qy      236 YYCNSRDRSSGNHV-VFGGGTKLTVLG 260
       :|||::|||::|||::|||::|||
Db      300 YFCGSYDRSSGYVIFGAGTTLTVLG 325

RESULT 6
US-10-512-184-64
; Sequence 64, Application US/10512184
; Publication No. US2005024901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F
; TITLE OF INVENTION: Antibodies, recombinant
; TITLE OF INVENTION: antibody fragments an
; TITLE OF INVENTION: resistance against f
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 327
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artifici
; OTHER INFORMATION: fusion protein compri
; OTHER INFORMATION: scFv CWPd2.
US-10-512-184-64

```

Query Match	46.7%	Score	672	DB 1	Length	327			
Best Local Similarity	56.0%	Pred. No.	2.7e-28						
Matches	149	Conservative	23	Mismatches	68	Indels	26	Gaps	8
Qy	16	AAQFAMAEVLVS	GGGVVRPGGSLRLSCAASGFTFDY	GMWSVRQAPGKGL	EWVSGINW	75			
Db	65	AAQFAMAAVTL	DES	GGGLQTPGGGLSVCKGSGFDFSS	DTMMVRQAPGKGL	EFVAGISG	124		
Qy	76	NGSGTYADSVK	GRFTISRDNAKNSLYLQNSLR	AEEDTAVY	CCARAPV	-----	125		
Db	125	DGSDTNYGSAV	KGRATISR	DNGOSTVRLQLNNLR	AEADTATYCT--RGPC	SPTKNCAADR	182		
Qy	126	--TWGGQTLTV	SRGG--GGSGGGGSGGG--	GSSELTQDP	PAVSVALGQTVRIT	CQGSLSLR	179		
Db	183	IDAWGHGTEVT	VSSGTS	SGSGKPGCEGSKGAPALTQPS	SVSANLGGTV	VEITCSGG--	239		
Qy	180	SYTASWVQOK--	PCQAPVLVLYGKN---	NBSGGLPDR	EGSSSGNTASLTITG	QAQAEAD	235		
Db	240	GTYRGFWQK	SGSAPVTVI	YDWDDBSANR	SPNIPSRFSGTSG	STATLTITGVQAD	299		
Qy	236	YYCNSRDS	SGNHV--VF	GGGTKLTVLG	260				
Db	300	YFCGSDYR	SSGYSIF	AGATTLTVLG	325				

```

RESULT 7
US-10-512-184-63
; Sequence 63, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.v.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```


FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising MBP - linker -
; OTHER INFORMATION: scFv PLPs.
US-10-512-184-72

Query Match 46.4%; Score 668.5; DB 1; Length 313;
Best Local Similarity 54.7%; Pred. No. 3.8e-28;
Matches 146; Conservative 29; Mismatches 67; Indels 25; Gaps 8;

Qy 16 AAQPAEAQLVVEGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVGINW 75
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
48 AAQPAEAQLVDESGGLQTPGGALSLVCKASGDFPKGYEMAWVRQAPGKLEWVAIS- 106
Qy 76 NGSSTGVADSVKGRFTISRDNKNSLYLQMSLRADETAVVYCARMAPV----- 125
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
107 SGYNWNTGAAVKGRATISRNNGQSTVRLQNLNRAEDTATYTCARHTGDYGCAGNWCSA 166
Qy 126 ----IWGGTGLTVTSRGG-GGSGGGGGGG---GSELTDPAVSVVALGQTVRITCOGDS 177
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
167 GNIDAWGHGTEVTSSGSGSGKPGEGSTKGAPGLTQASSVSANPGETVKTICSGG 226
Qy 178 --LRSYASVTQOK-PCQAPVLVYIGKNNRPSGIPDRFSGSSGNNTASLTITGAQAEDEA 234
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
227 SYAGSYTYGWTQKTPGSAPVTVIYSNDKRPSPNIPSRFSGSLSGSTNTLTITGVQVDEA 286
Qy 235 DYNCNSRDSGNHV-VFGGGLKLTVLG 260
Db ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
287 VYFCAYDN--NYAGIFGAGTTLTVLG 311

RESULT 11
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match 45.1%; Score 649.5; DB 1; Length 329;
Best Local Similarity 51.0%; Pred. No. 3.4e-27;
Matches 133; Conservative 43; Mismatches 70; Indels 15; Gaps 6;

Qy 16 AAQPAEAQLVVEGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVGINW 75
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
66 AAQPAEAQLVLESPELKKPGETVKISCKASGYTFKYGNWVVKQAPGKLGKMWGINT 125
Qy 76 NGSSTGVADSVKGRFTISRDNKNSLYLQMSLRADETAVVYCARMAPV-----INQOG 130
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
126 YTGEPVTADDPKGAPAFSLSTSTAPLIQNLNKNEDTATYFCARYGNPYTMDYWGQG 185
Qy 131 TLTVTSRGGGGGGGGGGGGSS--ELTQDP-AVSVVALGQTVRITCOGDSLSRSY-----Y 182
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
186 TSLTVSSGGGGGGGGGGGGSDIVLSQSPSLAVSVGEKVTMSCKSSQSLYSNNQNY 245
Qy 183 ASWTQKPGQAPVLVYIGKNNRPSGIPDRFSGSSGNNTASLTITGAQAEDEADYCNRSR 242
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||
246 LAWTQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGTDFTLTISSVKAEADLAVVYCCQYY 305

Qy 243 SSGNHVVFSGGTKLTVLGAAA 263
Db 306 S--YPFTFGSGTKLEIKRADA 324

RESULT 12
US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv CWPD2
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-26

Query Match 45.0%; Score 648; DB 1; Length 258;
Best Local Similarity 55.2%; Pred. No. 3.4e-27;
Matches 144; Conservative 23; Mismatches 68; Indels 26; Gaps 8;

Qy 21 MAEVLVVEGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVGINWNGST 80
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 MAATLDESQGLQTPGGGLSLVCKSGGDFSSDTMMWVRQAPGKLEFVAGISGDSGT 60
Qy 81 GYADSVKGRFTISRDNKNSLYLQMSLRADETAVVYCARMAPV-----IWG 128
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 NYGSVAVKGRATISRDNGQSTVRLQNLNRAEDTATYTC--RGPCSPYKNCADRIDA 118
Qy 129 QGTLTVTSRGG-GGSGGGGGGG---GSELTDPAVSVVALGQTVRITCOGDSLSRSYAS 184
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
119 HGTEVTSSGSGSGKPGEGSTKGAPALTQPSVSANLGGTVEITCSGG---GYRG 175
Qy 185 WYQOK-PCQAPVLVYIGKN---NRPGIPDRFSGSSGNNTASLTITGAQAEDEADYCN 240
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
176 WFQKSPGSAPVTVIYWDSDSANRPSNIPSRFSGSGTSGSTATLTITGVQADDEAVYFC 235
Qy 241 RDSGNHV-VFGGTKLTVLG 260
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
236 YDRSSGYVSIFGAGTTLTVLG 256

RESULT 13
US-10-512-184-35
; Sequence 35, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PLp9 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-35

Query Match          44.8%; Score 644.5; DB 1; Length 261;
Best Local Similarity 53.8%; Pred. No. 5.1e-27;
Matches 141; Conservative 29; Mismatches 67; Indels 25; Gaps 8;

Qy 21 MAEVLVESGGVVRPGGSLRLSCAASGFTDDYGMSSWVRQAPGKGLWVSGINWNGST 80
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAAVLDESGLLQTPGSLSLVCKASGDFPKGYEMAWVRQAPGKGLWVAALIS-SGYNT 59
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 81 GYADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRAPV-----I 126
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 NYGAAVGRATISRNNQSTVRLQNLNLRADETAIVYICAKTHGDCAGNWCAGNIDA 119
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 127 WGQGLTLTVSRGG-GSGGGGSGGG---GSELTQDPAVSVALGQTVRITCOGDS--LRS 180
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 WGHGTEVTVSSGTSSTGSGKPGGSGTGKAPGLTQASSVSANPGETVKITCSGGSVAGS 179
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 181 YYASWYQOK-PGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASITITGAQAEADYYCN 239
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 YYGYWYQKTPGSAPVTVIYNDKRPSPNIPSRFSGLSGSTNTLTITGVQVDDNAVYFCG 239
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 240 SRDSSGNHV-VFGGTTKLTVLIG 260
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 240 AYDN--NYAGIFAGTTLTVLG 259
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-10-512-184-29
; Sequence 29, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCES: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
US-10-512-184-29

Query Match          44.3%; Score 638.5; DB 1; Length 329;
Best Local Similarity 50.8%; Pred. No. 1.2e-26;
Matches 132; Conservative 42; Mismatches 72; Indels 15; Gaps 6;

Qy 16 AAQPMARVQLVRSGGVVRPGGSLRLSCAASGFTDDYGMSSWVRQAPGKGLWVSGINW 75
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 66 AAQPMARVQLVRSGGVVRPGGSLRLSCAASGFTDDYGMSSWVRQAPGKGLWVSGINW 75
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 76 NGGSTGYADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRA-PV-----IWGQG 130
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 126 YTGEPYVADDFKGRFAPSLSTSTAFQLQNNLNKEDTATYFCARYGNPYTMDYWGQG 185
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 131 TLVTVSRGGGSGGGSGGGSGGGSS-ELTQDP-AVSVALGQTVRITCOGDSLSRY-----Y 182
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 186 TSLTVSSGGGSGGGSGGGSGGGSDIVLSQSPSSLAVLVGKVTMCKSPQSGLLYSSNQNY 245
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 183 ASWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRD 242
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 246 LAMYQKPGQSPKLLIYMASTRSGVDPDRFTGSGSGTDFTLTISSVKAEADLAVYICQYY 305
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 243 SSGNHVVFSGGTTKLTVLGAAA 263
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 306 S--YPFTFGSGTKLEIKRADA 324
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Search completed: November 18, 2005, 22:18:07
Job time : 4.49527 secs

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```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PLp9 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-35

Query Match          44.8%; Score 644.5; DB 1; Length 261;
Best Local Similarity 53.8%; Pred. No. 5.1e-27;
Matches 141; Conservative 29; Mismatches 67; Indels 25; Gaps 8;

Qy 21 MAEVLVESGGVVRPGGSLRLSCAASGFTDDYGMSSWVRQAPGKGLWVSGINWNGST 80
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAAVLDESGLLQTPGSLSLVCKASGDFPKGYEMAWVRQAPGKGLWVAALIS-SGYNT 59
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 81 GYADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRAPV-----I 126
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 NYGAAVGRATISRNNQSTVRLQNLNLRADETAIVYICAKTHGDCAGNWCAGNIDA 119
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 127 WGQGLTLTVSRGG-GSGGGGSGGG---GSELTQDPAVSVALGQTVRITCOGDS--LRS 180
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 WGHGTEVTVSSGTSSTGSGKPGGSGTGKAPGLTQASSVSANPGETVKITCSGGSVAGS 179
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 181 YYASWYQOK-PGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASITITGAQAEADYYCN 239
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 YYGYWYQKTPGSAPVTVIYNDKRPSPNIPSRFSGLSGSTNTLTITGVQVDDNAVYFCG 239
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 240 SRDSSGNHV-VFGGTTKLTVLIG 260
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 240 AYDN--NYAGIFAGTTLTVLG 259
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-10-512-184-29
; Sequence 29, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCES: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SPIII7
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Mus musculus.
US-10-512-184-29

Query Match          44.5%; Score 641.5; DB 1; Length 263;
Best Local Similarity 53.1%; Pred. No. 7.2e-27;
Matches 138; Conservative 35; Mismatches 68; Indels 19; Gaps 8;

Qy 21 MAEVLVESGGVVRPGGSLRLSCAASGFTDDYGMSSWVRQAPGKGLWVSGINWNGST 80
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MAEVLVESGGVLRPGNSLKLSCVTSPTFSYRHMHLQPPGKRLWIAVIVKSEN 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 81 G--YADSVKGRFTISRDNKNSLYLQMSLRADETAIVYICARMRA-PV-----IWGQGLTVTS 136
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GADYAESVKGRFTISRDRSERSVYLQNLNLRADETAIVYICRSSESSEGFYWGQGLTVTS 120
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 137 RG---GGSGGGSG---GGSSSLTQDP-AVSVALGQTVRITCO-CDSL-----RSYYA 183
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 SGSTSGGKPGPGGSGTKGAPDIQMTQSPSLSVSAGEKVTLSCKSQSLLNSGNQCNFL 180
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 184 SWYQOKPGQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDS 243
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	643.5	44.7	268	2	A56446	Ig heavy chain V r
2	568	39.4	109	2	S19663	Ig lambda chain V r
3	565.5	39.3	249	2	S41374	single chain Fv an
4	562	39.0	108	2	S47184	Ig lambda chain -
5	551.5	38.3	110	2	S36272	Ig lambda chain V
6	546	37.9	127	2	S70444	Ig lambda chain pr
7	541	37.6	108	2	S38498	Ig lambda chain -
8	539	37.4	109	2	S38496	Ig lambda chain -
9	530.5	36.8	233	2	S25748	Ig lambda chain -
10	527	36.6	108	1	L3HUSH	Ig lambda chain V-
11	522.5	36.3	233	2	JCS322	p53 specific singl
12	518.5	36.0	110	2	S19672	Ig lambda chain V
13	518	36.0	146	2	S02083	Ig lambda chain V-
14	513	35.6	98	2	S29928	Ig heavy chain V r
15	510.5	35.5	128	2	S34595	Ig heavy chain V r
16	503	34.9	96	2	S36060	Ig lambda chain -
17	503	34.9	115	2	S13726	Ig lambda chain V
18	503	34.9	121	2	S31118	Ig heavy chain - h
19	502.5	34.9	233	2	S25741	Ig lambda chain -
20	502	34.9	123	2	S30532	Ig heavy chain V r
21	501	34.8	121	2	S31104	Ig heavy chain V r
22	495.5	34.4	112	2	PH1654	Ig heavy chain V r
23	491	34.1	120	2	S36273	Ig heavy chain V r
24	489.5	34.0	145	2	S11239	Ig heavy chain V r
25	489	34.0	134	2	S31699	Ig heavy chain V r
26	488	33.9	138	2	S31666	Ig heavy chain V r
27	486	33.8	160	2	S05271	Ig heavy chain pre
28	485.5	33.7	120	2	S41111	Ig heavy chain V-D
29	485	33.7	119	2	S31108	Ig heavy chain - h

A/Accession: S19663

A/Molecule type: mRNA

A/Residues: 1-109 <MAR>

A/Cross-references: UNIPARC:UPI0000039C3B; EMBL:X61640; NID:929492; PIDN:CAA43821.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 568; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.5e-31;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 SSELTPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 211

Db 1 SSELTPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60

Qy 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGKLTVLG 260

Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGKLTVLG 109

RESULT 3

S41374

single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

A/Accession: S41374

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <ART>

A/Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 39.3%; Score 565.5; DB 2; Length 249;

Best Local Similarity 48.2%; Pred. No. 5.2e-31;

Matches 123; Conservative 37; Mismatches 74; Indels 21; Gaps 6;

Qy 23 EVLVESGGGVPPGSLRLSCAASGFTFDYGMVSRQAPKGLVWSGNNWNGSTGY 82

Db 1 QVQLQSGAEVLPFGASVKLSTCTSGFNPKDDYIHWKQPEKLEWIAIPASGVKY 60

Qy 83 ADSVKGRFTISRDAKNSLYQNLSRAEDTAVYYCAR----MRAPVIMQGGTLTVTSRG 138

Db 61 VPRFQDKATITADTSSNTAYLLLSLTSEDTAVYYCARRDTLYTSLGYWGQGSTVTVSSR 120

Qy 139 GGGSGGGSGGGSS-ELTQD-PAVSVALGQTVRITCQ-----GDSLSRSYASWYQ 187

Db 121 GGGSGGGSGGGSGSDIELTQSPSPVVPVIGESVSISCRSKSLYSDGDS----YLFWFL 176

Qy 188 QKPGQAPVLVIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH 247

Db 177 QRFGQSPQLLIYRMSNLASGVDPDRFSGSGSGTFTLIRISVEAEADVGVYICMQRHRE--YP 234

Qy 248 VVFGGGKLTVLGAA 262

Db 235 LTFGAGTKLKLKRAA 249

RESULT 4

S47184

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S47184

R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

submitted to the EMBL Data Library, June 1994

A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient

A/Reference number: S47181

A/Accession: S47184

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 <NCI>

A/Cross-references: UNIPARC:UPI0000031AP6; EMBL:X79783; NID:9506426; PIDN:CAA56179.1; PII

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 562; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.7e-31;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 SSELTPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 211

Db 1 SSELTPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60

Qy 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGKLTVL 259

Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGKLTVL 108

RESULT 5

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C/Accession: S36272

R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.,

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MUID:93178448; PMID:7679990

A/Accession: S36272

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-110 <GRI>

A/Cross-references: UNIPARC:UPI0000118DP6; EMBL:Z18833; NID:G33419; PIDN:CAA79285.1; PID.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 551.5; DB 2; Length 110;

Best Local Similarity 98.2%; Pred. No. 1.9e-30;

Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 152 SSELTPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 211

Db 1 SSELTPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSPGIPDR 60

Qy 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN-HVVPFGGKLTVLG 260

Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNLYVVPFGGKLTVLG 110

RESULT 6

S70444

Ig lambda chain precursor V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004

C/Accession: S70444; S70426

R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A/Title: IgM kappa/lambda HBV human B cell clone: an early step of differentiation of fet

A/Reference number: S70442; MUID:93024508; PMID:1383695

A/Accession: S70444

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-127 <CUI>

A/Cross-references: UNIPROT:QNSD6; UNIPARC:UPI00000176807

A/Experimental source: clone E29.1

R/Tonnelle, C.

submitted to the EMBL Data Library, May 1990

A/Reference number: S70426

A/Accession: S70426

```

Query Match          37.4%; Score 539; DB 2; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.1e-29;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 152 SSELTDPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDR 211
DB 1 SSELTDPPAVSVALGQTVRITTCGDSLSKSYASWYQKPGQAPVLVYGNKNNRPSGIPDR 60

QY 212 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTTKLTIVLG 260
DB 61 FSGSYFGNTASLTITGAQAEDEADYYCTSRDTSGNHVLFGGTTKLTIVLG 109

RESULT 9
S25748
IG lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25748
R:Combiarto, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25748
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
C:Cross-references: UNIPARC:UPI000115BFC; EMBL:X57813; NID:G33725; PIDN:CAA409
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match          36.8%; Score 530.5; DB 2; Length 233;
Best Local Similarity 83.5%; Pred. No. 1.1e-28;
Matches 106; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

QY 152 SSELTDPPAVSVALGQTVRITTCGDSLSRSYASWYQKPGQAPVLVIYGNKNNRPSGIPDR 211
DB 20 SSELTDPPAVSVALGQTVRITTCGDSLSRYASWYQHKPGQAPILVIYGNKNNRPSGIPDR 79

QY 212 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTTKLTIVLG ---AAAEQKLI 268
DB 80 FSGSSGNTASPAITGAQAEDEADYYCNSRDSSGQVLFGGGTTKLTIVLGQPKAAPSVTLF 139

QY 269 --SEEDL 273
DB 140 PPSSEEL 146

RESULT 10
L3HUSH
IG lambda chain V-III region (Sh) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01980
R:Ritani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A:Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The
A:Reference number: A92057; MUID:70166723; PMID:4909564
A:Accession: A01980
A:Molecule type: protein
A:Residues: 1-108 <IT>
A:Cross-references: UNIPROT:P01714; UNIPARC:UPI000012B9FC
A>Note: the sequence of the C region is also given
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical l
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associat
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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F;14-88/Domain: immunoglobulin homology <IMM>
F;21-86/Disulfide bonds: #status experimental

Query Match 36.6%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 8.2e-29;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 153 SELTQDPVAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 212
DB 1 SELTQDPVAVSVALGQTVRITTCQDLSRGRDYAAMYQKPGQAPLVLYGKNNRPSGIPDRF 60

QY 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260
DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 108

RESULT 11

JC5322
P53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID: 97168950; PMID: 90167575
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Cross-references: UNIPARC:UPI000017C2DE
A;Experimental source: hybridoma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 36.3%; Score 522.5; DB 2; Length 233;
Best Local Similarity 49.0%; Pred. No. 3.6e-28;
Matches 117; Conservative 32; Mismatches 75; Indels 15; Gaps 8;

QY 28 ESGGVVRPGSLRLSCAASGFTDDYGMNWVROAPKGLSWGGINWGGSTGYADSVK 87
DB 2 ESGAELVRSGASVKLSCTTGFINDIYMHVWVKRPEQGLEIGRIDPENGADMTRSSG 61

QY 88 GRPTISRDNAKNSLYLQWNSLRARDTAVYVC-AMRAPVTVGQGTTLTVSRGGSGGGG 146
DB 62 VKATWTADTSNTAYLQLSLTSETAVYCNAGMD---YAGQGTTVTVSGGGSGSGRA 118

QY 147 SGGGSS-ELTQDPA-VSVALGQTVRITTCQD---SLRSY-YASWYQKPGQAPLVLYG 200
DB 119 SGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQKPGQPPRLIYL 178

QY 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYYC-NSRDSSGNHVVFGGTKLTV 258
DB 179 VSNLESGVPARFSGSGSGTDTFLNHPVBEADAATYYCQHIRELTRSE---GGTKLEI 233

RESULT 12

S19672
Ig lambda chain V region (clone alpha-TSL14) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19672
R;Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID: 92085276; PMID: 1748994
A;Accession: S19672
A;Molecule type: mRNA
A;Residues: 1-110 <MAR>
A;Cross-references: UNIPARC:UPI0000115FE3; EMBL:X61644; NID:937856; PIDN:CAA43825.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 36.0%; Score 518.5; DB 2; Length 110;

Best Local Similarity 91.8%; Pred. No. 3.1e-28;
Matches 101; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 152 SSELTDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDR 211
DB 1 SSELTDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260
DB 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 110

RESULT 13

S02083
Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N;Alternate names: amyloid-fibril protein GIL
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02083
R;Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
Biochem. J. 256, 973-980, 1988
A;Title: The primary structure of the variable region of an immunoglobulin IV light-chain
A;Reference number: S02083; MUID: 89134210; PMID: 3146981
A;Accession: S02083
A;Molecule type: protein
A;Residues: 1-70171-72173-75;76-131;132-146 <FYK>
A;Cross-references: UNIPARC:UPI0000176830; UNIPARC:UPI0000176831; UNIPARC:UPI0000176832;
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>

Query Match 36.0%; Score 518; DB 2; Length 146;
Best Local Similarity 82.7%; Pred. No. 4.5e-28;
Matches 105; Conservative 8; Mismatches 8; Indels 6; Gaps 3;

QY 153 SELTDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 212
DB 1 SELTDPAVSVAGQTVRITTCQDLSRNFVAFVYQKPGQAPLVLYGKNNRPSGIPBRF 60

QY 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVFGGTKLTVLG---AAAEQKLI 268
DB 61 SGSSSGNTASLTITGAQAEADYYCNSRNSGNHYHVGFGTKLTVLSQPKAAPSVTLF 120

QY 269 --SEEDL 273
DB 121 PPSSEEL 127

RESULT 14

S26928
Ig heavy chain V region (DP-32) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26928
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26985; MUID: 93021117; PMID: 1404388
A;Accession: S26928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000116409; EMBL:Z12334; NID:932887; PIDN:CAA78204.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 35.6%; Score 513; DB 2; Length 98;
Best Local Similarity 98.0%; Pred. No. 6.4e-28;
Matches 96; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 23 EVOLVESGGVVRPGGSLRLSCAASGFTDDYGMNWVROAPKGLSWGGINWGGSTGY 82
|||||

Db 1 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 60
Qy 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR 120
Db 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTALYHCAR 98

RESULT 15
S31595
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31595
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31595
A:Accession: S31595
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <CUI>
A:Cross-references: UNIPARC:UPI0000116458; EMBL:Z14171; NID:g31007; PIDN:CAA78540.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;23-106/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 510.5; DB 2; Length 128;
Best Local Similarity 83.3%; Pred. No. 1.2e-27;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;

Qy 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 82
Db 9 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 68

Qy 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMAP-----VINGQGLVTVS 136
Db 69 ADSVKGRFTISRDNKNSLYLQMSLRAEDTALYCAK-DAPGDHDAFDINGQGLVTVS 127

Search completed: November 18, 2005, 21:47:22
Job time : 28.0883 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:35:09 ; Search time 158.161 Seconds
(without alignments)
1235.649 Million cell updates/sec

Title: US-10-029-926d-25
Perfect score: 1440
Sequence: 1 MKYLLPTAARGLLLAQA.....VLGAARQLISBEDINGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	758	52.6	240	2	Q65ZC9 HUMAN
2	715	49.7	255	2	Q6KB05 mus musculus
3	695.5	48.3	248	2	Q65Z07 MUR1
4	636	44.2	244	2	Q65ZC8 HUMAN
5	600	41.7	241	2	Q65ZC8 HUMAN
6	578	40.1	243	2	Q65ZC8 HUMAN
7	552	38.3	107	2	Q65ZC8 HUMAN
8	550.5	38.2	112	2	Q65ZC8 HUMAN
9	548	38.1	487	2	Q65ZC8 HUMAN
10	530	36.8	233	2	Q65ZC8 HUMAN
11	527	36.6	108	1	LV3A HUMAN
12	516	35.8	472	2	Q6N089 HUMAN
13	511	35.5	499	2	Q6N5K4 HUMAN
14	509.5	35.4	469	2	Q659F4 HUMAN
15	508	35.3	573	2	Q6WU38 HUMAN
16	507.5	35.2	218	2	Q625S1 MOUSE
17	504	35.0	97	2	Q6N773 HUMAN
18	483	33.5	121	2	Q6UL71 HUMAN
19	478	33.2	470	2	Q6PJ44 HUMAN
20	478	33.1	478	2	Q6PI81 HUMAN
21	477	33.1	606	2	Q6GMV2 HUMAN
22	474	32.9	464	2	Q6MZU6 HUMAN
23	474	32.9	613	2	Q6WUK1 HUMAN
24	473.5	32.9	597	2	Q66BB9 HUMAN
25	471.5	32.7	473	2	Q6MZV7 HUMAN
26	470	32.6	113	2	Q6UL90 HUMAN
27	465	32.3	493	2	Q6GMX2 HUMAN
28	461.5	32.0	118	2	Q6UL91 HUMAN
29	457.5	31.8	475	2	Q6MZQ6 HUMAN
30	456	31.7	466	2	Q6IN78 HUMAN
31	452.5	31.4	479	2	Q6MZV6 HUMAN

32	451.5	31.4	467	2	Q4VBH1 RAT
33	450	31.2	473	2	Q91205 mus musculus
34	448.5	31.1	465	2	Q6P6C4 HUMAN
35	448	31.1	461	2	Q5M7V3 RAT
36	446.5	31.0	116	1	HV3T HUMAN
37	446.5	31.0	465	2	O510J0 RAT
38	446.5	31.0	494	2	Q6ZM64 HUMAN
39	445	30.9	479	2	Q91WP5 mus musculus
40	444.5	30.9	122	1	HV3G HUMAN
41	444	30.8	116	2	Q9UL93 HUMAN
42	443	30.8	117	1	HV3C HUMAN
43	443	30.8	479	2	Q5PQK9 RAT
44	442.5	30.7	475	2	Q5EFES HUMAN
45	441.5	30.7	494	2	Q96K68 HUMAN

ALIGNMENTS

RESULT 1

Q65ZC9 HUMAN
ID Q65ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific antibodies."
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 52.6%; Score 758; DB 2; Length 240;
Best Local Similarity 62.9%; Pred. No. 5.2e-47;
Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;

Qy	23	EVOLVESGGGVAPRGSSRLSCAASGTFDDYGMVSRQAPGKLEWVSGINWNGSTGY	82
Db	1	QVQLVQSGGGLVQPGGSLRLSCAASGTFPSYGMHWVRQAPGKLEWVAIVSYDGSNKYY	60
Qy	83	ADSVKGRFTISRDNAKNSLYQMNSLRRAEDTAVYICARMRAPVI--WGQGTLTIVTSRGGG	140
Db	61	ADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVYICARDWDGSDLPNGKGLTIVTSRGGG	120
Qy	141	GSGGGGSGGGSS--ELTQDPA-VSVALGQVTRITCQGDLSRYSYASVYQKPGQAPLVVI	198
Db	121	GSGGGGSGGGSDIQMTQSPSTLSASITGDRVTITCRASEGIYRWLAIVYQKPGKAPKLLI	180
Qy	199	YGNKNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFVGGGTGLTV	258
Db	181	YKASSLASRAPSPRPSGGSGGTDFLTITSSLPQDDFATYYC--QQYSNYPTFGGTTKLEI	238

RESULT 2

QY 23 EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSTWRQAPGKGLEWVSGINWNGGSTGY 82

```

RESULT 7
Q9NSD6_HUMAN
ID Q9NSD6_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Homo sapiens This CDS feature is included to show the translation of
DE the corresponding V region. Presently translation qualifiers on
DE V region features are illegal. (Fragment).
GN Name=IGLV3-19;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymphocyte;
RA Hohmann A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1383695;
RX Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;
RT "IGM kappa/lambda BBV human B cell clone: an early step of
RT differentiation of fetal B cells or a distinct B lineage?";
RL Mol. Immunol. 29:1363-1373(1992).
DR EMBL; LA3092; AAA69746.2; -; mRNA.
DR PIR; S70444; S70444.
DR HSP; P01709; 2MCG.
DR HGNC; HGNC:5903; IGLV3-19.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
FT SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 38.3%; Score 552; DB 2; Length 107;
Best Local Similarity 98.1%; Pred. No. 1.7e-32;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 ELTQDPVAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLVIYKNNRPSGIPDRPS 213
Db 1 ELTQDPVAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLVIYKNNRPSGIPDRPS 60

Qy 214 GSSSGNTASLTITGAQADEADYYCNSRDSGNHVFVGGGKLTVLG 260
Db 61 GSSSGNTASLTITGAQADEADYYCNSRDSGNHVFVGGGKLTVLG 107

RESULT 8
Q9HCC1_HUMAN
ID Q9HCC1_HUMAN PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -; mRNA.
DR HSP; P01783; 1IGC.
DR BMR; Q9HCC1; 1-112.

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DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-Like.
DR SMART; SM003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
FT SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 38.2%; Score 550.5; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 2.3e-32;
Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 23 EVOLVESGGVVRPGGSLRLSCAASGFTFDDYGMVSRQAPGKLEWVGGINWGGSTGY 82
Db 1 EVOLVESGGVVRPGGSLRLSCAASGFTFDDYGMVSRQAPGKLEWVGGINWGGSTGY 60

Qy 83 ADSVKGRFTISRDNKNSLYLQNSLRARDTAVYYCARMR-APVIWGGQTLV 133
Db 61 ADSVKGRFTISRDNKNSLYLQNSLRARDTAVYYCARRRYALDYWGQGTLLV 112

RESULT 9
Q65ZL2_9MURI
ID Q65ZL2_9MURI PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN- $\tau$ ;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003598; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 38.1%; Score 548; DB 2; Length 487;
Best Local Similarity 45.6%; Pred. No. 1.9e-31;
Matches 109; Conservative 45; Mismatches 79; Indels 6; Gaps 5;

Qy 22 AEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMVSRQAPGKLEWVGGINWGGSTG 81
Db 19 SQVQLQDSADSLVKGASVKISCKASGYTFTDRIHWAKQKPGQGLEWYISPGNDIK 78

Qy 82 YADSVKGRFTISRDNKNSLYLQNSLRARDTAVYYCARMR-APVIWGGQTLVTSRGGG 141
Db 79 YNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRSYYG-HWGQGTTLTGS-GGGG 136

Qy 142 SGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLVIY

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Db 137 SGGGSGGGGRIGQWTSQASLSVSVGLVITTCRASENIYSNLAWYQKQKSPQLIVY 196
Qy 200 GKNNRPSGIPRFGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTV 258
Db 197 AATNLADGVPFRFGSGSGTQYSLKNSLQSEDGSIYC--QHWGTPTPTFGGTRLEI 253

RESULT 10
Q6GMW4 HUMAN
ID Q6GMW4 HUMAN PRELIMINARY; PRT; 233 AA.
AC Q6GMW4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haiech P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073786; AAH73786.1; -, mRNA.
DR SMR; Q6GMW4; 23-229.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5BD CRC64;
```

```
Query Match 36.8%; Score 530; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 1.6e-30;
Matches 100; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 152 SSELTPDAVSVALGQTVRITTCQGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDR 211
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Db 20 SSELTPDAVSVALGQTVRITTCQGDSLSRTTYASWYQKPGQAPVLVIYGNRPSGIPDR 79
Qy 212 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260
Db 80 FSGSGSGNTASLTITGAQAEADYYCNSRDSSGSHLVFGGTGKTVTLG 128

RESULT 11
LV3A HUMAN
ID LV3A HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RA "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176(1970).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01980; L3HUSH.
DR HSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 97 IG-like.
FT DISULFID 21 86
FT NON_TER 108 108
FT SQ SEQUENCE 108 AA; 11393 MW; E7E1229586411A56 CRC64;

Query Match 36.6%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 1.1e-30;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 153 SELTPDAVSVALGQTVRITTCQGDSLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Db 1 SELTPDAVSVALGQTVRITTCQGDSLSRGYDAAWYQKPGQAPVLVIYGNRPSGIPDRF 60

Qy 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260
Db 61 SGSSSGHTASLTITGAQAEADYYCNSRDSSGKHLVFGGTGKTVTLG 108

RESULT 12
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFp686f15220.
GN Name=DKFp686f15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Wewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BK640627; CAB45781.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 35.8%; Score 516; DB 2; Length 472;
Best Local Similarity 47.3%; Pred. No. 3.7e-29;
Matches 116; Conservative 20; Mismatches 77; Indels 32; Gaps 5;

QY 13 LLIAQAPAMAEVOLVESGGVVRPGSLRLSCAASGFTDDYGMVWRQAPGKLEWVSG 72
DB 10 LLAILGVQCEVLVESGGVVRPGSLRLSCAASGFTDDYGMVWRQAPGKLEWVSG 69

QY 73 INWGGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICAR-----MRAP 124
DB 70 ISWNSGSIAYADSVKGRFTISRDNKNSLYLQNSLRAEDTALYCAKEIGHNFFYYGM 129

QY 125 VINGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 184
DB 130 DVWVGQGLTVTVS-----SASTKGPSVFPLAPSSKSTSGGTAALGCL--LVKDYFPE 177

QY 185 WYQKPGQAPRVLYIGKNNRPSGI---PDRFSGSSSGNTASLITGAQAEDEADYYCNSR 241
DB 178 -----PVTVSNWNGALTSVHTFPAVLQSSGLYSLSSVTVFVSSSLGTQTYICNVN 228

QY 242 DSSGN 246
DB 229 HKPSN 233

RESULT 13
ID Q8NSK4_HUMAN PRELIMINARY; PRT; 499 AA.
AC Q8NSK4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

```

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skaleks U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -; mRNA.
DR HSSP; P01876; 1OW0.
DR SMR; Q8NSK4; 269-477.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain; Repeat.
SQ
SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 35.5%; Score 511; DB 2; Length 499;
Best Local Similarity 49.6%; Pred. No. 9.1e-29;
Matches 121; Conservative 16; Mismatches 49; Indels 58; Gaps 8;

QY 13 LLIAQAPAMAEVOLVESGGVVRPGSLRLSCAASGFTDDYGMVWRQAPGKLEWVSG 72
DB 10 LLAILGVQCEVLVESGGVVRPGSLRLSCATSGFTDDSDGASWVRQAPGKLEWVSS 69

QY 73 INWGGSTGYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICARWAPV----- 125
DB 70 INWGGSTGYADSVKGRFTISRDNKNSLYLQNSLRLVEDTALYICARDPTKYCSGGSCL 129

QY 126 ----IWGQGLTVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 173
DB 130 GYMDVWVGKTVTVS-----SASPTSPKVPFLSLCSTQPDGNVVLACL 174

QY 174 QGDSLASYASWYQQKP-----GQAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTI 225
DB 175 QG-----FPQEPFLSVTVSSESGG---VTARNFFPS---QDASGDLYTTSQTL 218

QY 226 TGAQ 229
DB 219 PATQ 222

RESULT 14
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.

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```

GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC092518; AHH52518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 35.4%; Score 509.5; DB 2; Length 469;
Best Local Similarity 48.3%; Pred. No. 1.1e-28;
Matches 117; Conservative 20; Mismatches 76; Indels 29; Gaps 5;

Qy 13 LLLAAQPMAEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMYSWRQAPGKLEWVS 72
Db 10 LVAILKGQCEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMYSWRQAPGKLEWVS 69

Qy 73 INWNGSGTYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICARMAPV-----IW 127
Db 70 ISWDGGSTYYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICATRGGYTAGPDY 129

Qy 128 GQGLTVTVSRGGGSGGGGSGGSELTDPAVSVVALGQTVRITCQDLSRLSYASWYQ 187
Db 130 GQGLTVTVS-----SASTKGPSVPLAPSKSTSGTALGC---LVKDYFPE--- 174

Qy 188 QKPGQAPVLYVYGNRRPSGI---PDRFSGSSSGNTASLTITGAQADEADYYCNSRDS 244
Db 175 -----PVTWSNWSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQYICNVNHP 228

Qy 245 GN 246
Db 229 SN 230

RESULT 15
Q8WU38_HUMAN
ID Q8WU38 HUMAN PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH protein.
GN Name=IGHD;
OS Homo sapiens (Human).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RL immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345(1992).
DR ENBL; BC021276; AHH21276.1; -; mRNA.
DR PIR; S21205; S21205.
DR HSP; P18529; I18K.
DR Ensembl; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 35.3%; Score 508; DB 2; Length 573;
Best Local Similarity 48.4%; Pred. No. 1.8e-28;
Matches 119; Conservative 18; Mismatches 61; Indels 48; Gaps 6;

Qy 13 LLLAAQPMAEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMYSWRQAPGKLEWVS 72
Db 10 LVAILKGQCEVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMYSWRQAPGKLEWVS 69

Qy 73 INWNGSGTYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICARMAPV----- 125
Db 70 ISWNGSGTYADSVKGRFTISRDNKNSLYLQNSLRAEDTAVYICAKHGSGYIGYYG 129

Qy 126 --IWGQGLTVTVSRGGGSGGGGSGGSELTDPAVSVVAL-----GQTVRITC-- 173
Db 130 MDVWVGQGLTVTV-----SSAPTKAPDVPFPIISGCRHPKDNPSVVLACLI 173

```

Qy	174	QGBSLRSYVASWYQKPGQAPVLVIYKNNRPS-GIPDREGSSGNTASLTITGAQAE	232
Db	174	TGYHTSVTVIWM-----GTQSQPORTPFIQRRDSYMYTSSQLSTPLQQR	221
Qy	233	EADYYC	238
Db	222	QBEYKC	227

Search completed: November 18, 2005, 21:53:33
Job time : 160.161 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:17:08 ; Search time 61.6278 Seconds
(without alignments)
791.381 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576

Sequence: 1 SELTQDPASVALQQTVRIT.....SGNHWFGGKTLTLVGLAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	5	Abg78132 Human Fv
2	576	100.0	111	5	Abg91823 Human ant
3	576	100.0	112	8	Adj57867 Common li
4	576	100.0	125	9	Adw88761 Hepatitis
5	576	100.0	209	5	Aau98017 Human ace
6	576	100.0	244	9	Adw90315 Phage scf
7	576	100.0	244	9	Adx01815 SARS coro
8	576	100.0	247	9	Adw90312 Phage scf
9	576	100.0	247	9	Adx01809 SARS coro
10	576	100.0	249	8	Adr23324 Human CD7
11	576	100.0	260	5	Abg92023 Antibody
12	576	100.0	263	5	Abg92024 Antibody
13	576	100.0	266	5	Abg92020 Human ant
14	576	100.0	277	5	Abg78150 Human Fv
15	576	100.0	277	5	Abg78328 Human Fv
16	576	100.0	277	5	Abg92019 Human ant
17	576	100.0	277	5	Abg91841 Human ant
18	576	100.0	277	8	Adi28366 Human scf
19	576	100.0	277	8	Adw82026 Human pla
20	576	100.0	278	8	Adi28367 Human scf
21	576	100.0	278	8	Adw82027 Human pla
22	576	100.0	280	4	Aae02186 PAM2 sing
23	576	100.0	280	8	Adi28368 Human scf
24	576	100.0	280	8	Adj57363 P-selecti

25	576	100.0	280	8	AdS82028 Human leu
26	576	100.0	280	8	AdT63078 Human scf
27	576	100.0	280	9	Adx01180 Amino aci
28	576	100.0	280	9	Adx01181 Amino aci
29	576	100.0	280	9	Adx01131 Amino aci
30	576	100.0	280	9	Adx01130 Amino aci
31	576	100.0	280	9	Adx01185 Amino aci
32	576	100.0	280	9	Adx01186 Amino aci
33	576	100.0	280	9	Ady78380 Single ch
34	576	100.0	280	9	Ady78325 Single ch
35	576	100.0	280	9	Ady78324 Single ch
36	576	100.0	280	9	Ady78379 Single ch
37	576	100.0	280	9	Ady78374 Single ch
38	576	100.0	280	9	Ady78375 Single ch
39	576	100.0	282	4	AAE02185 PAM1 sing
40	576	100.0	309	2	AAW83322 Single ch
41	576	100.0	309	5	ABB09603 Amino aci
42	576	100.0	309	6	ABG74384 Single ch
43	576	100.0	309	7	ADG98737 Human sin
44	576	100.0	309	8	ADO40446 Human sin
45	576	100.0	312	2	AAW83323 Single ch

ALIGNMENTS

RESULT 1

ABG78132

ID ABG78132 standard; protein; 111 AA.

XX AC ABG78132;

XX XX

DT 15-NOV-2002 (first entry)

XX XX

DE Human Fv molecule hypervariable region related peptide #7.

XX XX

KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX XX

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.

XX PS Disclosure; Page 150; 232pp; English.

XX XX

CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCQDLSRSYASMTYQKPGQAPVLVIYGNRRPSGIPDRF 60
 DB 1 SELTQDPAVSVALGQTVRITCQDLSRSYASMTYQKPGQAPVLVIYGNRRPSGIPDRF 60
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111

RESULT 2

ABG91823
 ID ABG91823 standard; protein; 111 AA.

XX ABG91823;

DT 04-DEC-2002 (first entry)

XX Human antibody fragment #7.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
 XX Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

XX Disclosure; Page 227-228; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing

CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCQDLSRSYASMTYQKPGQAPVLVIYGNRRPSGIPDRF 60
 DB 1 SELTQDPAVSVALGQTVRITCQDLSRSYASMTYQKPGQAPVLVIYGNRRPSGIPDRF 60
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 DB 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111

RESULT 3

ADJ57867

ID ADJ57867 standard; protein; 112 AA.

XX ADJ57867;

XX 06-MAY-2004 (first entry)

XX Common light variable chain protein of B28, II-2 and I-2.

XX Cytostatic; Immunosuppressive; Antibacterial; Virucide; Fungicide;
 KW Antiparasitic; auto-immune disease; cancer; neoplastic disorder;
 KW leukaemia.

XX Synthetic.

XX WO2004009618-A2.

XX 29-JAN-2004.

XX 15-JUL-2003; 2003WO-EP007690.

XX 18-JUL-2002; 2002EP-00077953.

XX 18-JUL-2002; 2002US-0397066P.

XX 27-MAY-2003; 2003WO-EP050201.

XX (CRUC-) CRUCELL HOLLAND BV.

XX Van Berkel PHC, Brus RHP, Bout A, Logtenberg T;
 PI WPI; 2004-132914/13.

XX N-PSDB; ADJ57866.

XX Producing mixture of antibodies in recombinant host comprises expressing
 PT nucleic acid sequence(s) encoding light chain and three different heavy
 PT chains capable of pairing with light chain in recombinant host cell.

XX Disclosure; SEQ ID NO 18; 186pp; English.

XX The present invention relates to producing a mixture of antibodies in a
 CC recombinant host comprises expressing in a recombinant host cell a
 CC nucleic acid sequence or nucleic acid sequences encoding a light chain
 CC and at least three different heavy chains that are capable of pairing
 CC with a light chain. The method is useful for producing a mixture of
 CC antibodies in a recombinant host, is useful for the preparation of a
 CC medicament for use in the treatment or diagnosis of a disease or disorder

CC in a human or animal. The antibodies are useful for treating auto-immune
 CC disease and cancer such as solid tumors of the brain, head and neck,
 CC breast, prostate, colon, lung, etc., hematologic tumors such as B-cell
 CC tumors, neoplastic disorders such as leukemia, lymphoma, sarcoma,
 CC carcinoma, neural cell tumors, myelomas, melanomas, neuroblastomas, etc,
 CC and are also useful for treating graft-versus-host rejections, infectious
 CC diseases due to pathogenic bacteria such as multidrug resistant
 CC Staphylococcus aureus, fungi such as Candida albicans, as prophylaxis
 CC against viruses such as rabies virus, for treating or preventing disease
 CC caused by adenoviruses, respiratory syncytium virus, and for treating
 CC diseases caused by unicellular or multicellular parasites. The method
 CC enables exploring many combinations simultaneously, where the
 CC combinations include the presence of bispecific antibodies in the
 CC produced mixture. The present sequence represents the common light
 CC variable chain of B28, II-2 and I-2.
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 576; DB 8; Length 112;
 Best Local Similarity 100.0%; Pred. No. 3.2e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 2 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 61
 QY 61 SGSSSGNTASLITITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAA 111
 DB 62 SGSSSGNTASLITITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAA 112

RESULT 4
 ADW88761
 ID ADW88761 standard; protein; 125 AA.
 XX
 AC ADW88761;
 XX
 XX 07-APR-2005 (first entry)
 XX Hepatitis B virus surface antigen scFv antibody.
 XX
 KW Analyte detection; microarray; hepatitis B virus surface antigen;
 KW single chain antibody; heavy chain variable region.
 XX
 OS Unidentified.
 XX
 XX W02005007893-A2.
 XX
 XX 27-JAN-2005.
 XX
 XX 09-JUL-2004; 2004WO-US021765.
 XX
 XX 10-JUL-2003; 2003US-0487018P.
 XX 06-OCT-2003; 2003US-0509196P.
 XX
 XX (BLIN-) BLIND PIG PROTEOMICS LLC.
 XX
 XX Cull MG, Brennan M, Gill R;
 XX
 XX WPI; 2005-152093/16.
 XX N-PSDB; ADW88759, ADW88760.
 XX
 XX Detecting binding, useful for detecting antigen:antibody complexes, by
 XX providing Physically Alterable Binding Reagent and ligand, and detecting
 XX conformational change in Physically Alterable Binding Reagent to detect
 XX binding to the ligand.
 XX
 XX Example 7; SEQ ID NO 8; 37pp; English.
 XX
 XX The invention relates to a universal detection system for ligand binding
 XX using a physically alterable binding reagent (PABR) and in some
 XX embodiments a universal detection reagent (UDR). A claimed method for
 XX detection of binding comprises: providing a PABR; providing a ligand,

CC where the PABR specifically binds to the ligand; and detecting a
 CC conformational change in the PABR, whereby binding of the PABR to the
 CC ligand is detected. The conformational change may be detected by:
 CC providing a UDR; and detecting binding of the UDR to the PABR. The
 CC detection may be quantitative. The PABR may comprise: a ligand binding
 CC site; a domain that becomes physically altered upon binding of ligand to
 CC the ligand binding site; and, optionally, a site useful for coupling the
 CC binding reagent to a solid support. The PABR may comprise an antibody or
 CC a receptor binding domain or a tag for coupling the PABR to a solid
 CC support. The antibody may be a monomeric IgM, oligomeric IgW, an Fab
 CC fragment, an F(ab)2 fragment, a genetically engineered antibody or a
 CC chimeric antibody. A further method for detecting binding comprises:
 CC preparing a microarray comprising a plurality of PABRs at specific
 CC locations on the surface of a solid support in an addressable format;
 CC providing a sample suspected of containing a ligand such that the PABR
 CC specifically binds to the ligand; providing a UDR; and detecting the
 CC binding of the UDR to the PABR. The methods are useful for detecting
 CC ligand binding, e.g. as diagnostics, research uses, and industrial
 CC applications. The methods are also useful in detecting antigen:antibody
 CC complexes on either protein or antibody microarrays. The present sequence
 CC is that of the light chain variable region of a hepatitis B virus surface
 CC antigen (HBsAg) single chain Fv antibody. An AvidTagged IgM antibody
 CC suitable for use as a PABR could be constructed using the variable heavy
 CC chain domain sequence and a light chain domain sequence (variable and
 CC constant regions) that together contain the HBsAg antibody domains.
 XX
 SQ Sequence 125 AA;

Query Match 100.0%; Score 576; DB 9; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.6e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 QY 61 SGSSSGNTASLITITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAA 111
 DB 61 SGSSSGNTASLITITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAA 111

RESULT 5
 AAU98017
 ID AAU98017 standard; protein; 209 AA.
 XX
 AC AAU98017;
 XX
 XX 27-AUG-2002 (first entry)
 XX Human acetylcholinesterase antibody PD-antiHASP 1.
 XX
 XX Human; synaptic acetylcholinesterase; PD-antiHASP 1; antibody;
 KW single-chain variable fragment; scFv; AChE-S;
 KW heavy chain variable region; progressive neuromuscular disorder;
 KW muscle distortion; muscle re-innervation; myasthenia gravis;
 KW neuromuscular junction abnormality; Eaton-Lambert disease;
 KW muscular dystrophy; amyotrophic lateral sclerosis; ALS;
 KW post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
 KW post-stroke sclerosis; post-injury muscle damage;
 KW excessive re-innervation.
 XX
 OS Homo sapiens.
 XX
 XX W0200246422-A1.
 XX
 XX 13-JUN-2002.
 XX
 XX 22-MAY-2001; 2001WO-IL000464.
 XX
 XX 04-DEC-2000; 2000IU-00140071.
 XX
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX

PI Soreq H, Flores CF, Nissim A;
 XX WPI; 2002-463832/49.
 DR N-PSDB; ABK52915.
 XX
 XX Nucleic acid sequence coding for a single-chain variable fragment (scFv)
 PT antibody that has specific affinity for the synaptic variant of
 PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular
 PT disorder, e.g. Myasthenia gravis.
 XX
 XX Claim 11; Page 61-63; 73pp; English.
 PS
 XX The invention relates to a nucleic acid sequence coding for a single-
 CC chain variable fragment (scFv) antibody that has specific affinity for
 CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv
 CC antibody consists essentially of a polypeptide comprising the binding
 CC portion of the heavy chain variable region of an antibody. Also included
 CC are an expression vehicle comprising a nucleic acid sequence coding for a
 CC scFv antibody that has specific affinity for the synaptic variant of AChE
 CC -S, an scFv antibody specifically recognising and binding to the synaptic
 CC variant of AChE-S and a method for the diagnosis of a progressive
 CC neuromuscular disorder in a mammal, comprising obtaining a sample from
 CC the mammal and detecting intensified expression of at least one of the
 CC AChE variants in the sample. The single-chain Fv antibody is useful for
 CC diagnosing a progressive neuromuscular disorder which involves any one of
 CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
 CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
 CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
 CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post
 CC stroke sclerosis, post-injury muscle damage, excessive re-innervation,
 CC or post-exposure to AChE inhibitors. The present sequence represents an
 CC anti-AChE scFv antibody, PD-antiHASP 1
 XX
 SQ Sequence 209 AA;
 Query Match 100.0%; Score 576; DB 5; Length 209;
 Best Local Similarity 100.0%; Pred. No. 6e-35;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 60
 Db 76 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 135
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 Db 136 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 186
 RESULT 6
 ADW90315
 ID ADW90315 standard; protein; 244 AA.
 XX
 AC ADW90315;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Phage scFv SARS antibody SEQ ID NO 585.
 XX
 XX Virucide; Vaccine; diagnosis; Severe acute respiratory syndrome;
 KW respiratory-gen.; infection; respiratory disease; antibody.
 KW SARS coronavirus.
 OS
 PN WO2005012337-A2.
 XX
 XX 10-FEB-2005.
 XX
 XX 15-JUL-2004; 2004WO-EP051498.
 XX
 PR 15-JUL-2003; 2003WO-EP050308.
 PR 24-JUL-2003; 2003WO-EP050333.
 PR 02-SEP-2003; 2003WO-EP050392.
 PR 27-OCT-2003; 2003WO-EP050761.

PR 24-NOV-2003; 2003WO-EP050883.
 XX
 PA (CRUC-) CRUCELL HOLLAND BV.
 XX
 PI Ter Meulen JH, Goudmit J, Slootstra JW, Timmerman P, De Kruif CA;
 PI Van Den Brink EN;
 XX WPI; 2005-162947/17.
 XX
 XX New antigenic peptides from severe acute respiratory syndrome-coronavirus
 PT (SARS-CoV), useful in preparing a composition for diagnosing, treating or
 PT preventing SARS-CoV infection.
 XX
 XX Example 2; SEQ ID NO 585; 199pp; English.
 PS
 XX The invention relates to an antigenic peptide from severe acute
 CC respiratory syndrome-coronavirus (SARS-CoV). The peptide or nucleic acid
 CC molecule encoding the peptide, fusion protein, conjugate or antibody is
 CC useful in preparing a composition for diagnosing, treating or preventing
 CC SARS-CoV infection. The present sequence represents a phage scFv SARS
 CC antibody.
 XX
 SQ Sequence 244 AA;
 Query Match 100.0%; Score 576; DB 9; Length 244;
 Best Local Similarity 100.0%; Pred. No. 7e-35;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 60
 Db 134 SELTQDPAVSVALGQTVRIITCQGSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF 193
 QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
 Db 194 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 244
 RESULT 7
 ADX01815
 ID ADX01815 standard; protein; 244 AA.
 XX
 AC ADX01815;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE SARS coronavirus scFv antibody SEQ ID NO 71.
 XX
 KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody.
 XX
 OS SARS coronavirus.
 OS
 PN WO2005012360-A2.
 XX
 XX 10-FEB-2005.
 XX
 XX 21-JUL-2004; 2004WO-EP051568.
 XX
 XX 22-JUL-2003; 2003WO-EP050328.
 PR 01-SEP-2003; 2003WO-EP050391.
 PR 16-OCT-2003; 2003WO-EP050723.
 PR 24-NOV-2003; 2003WO-EP050883.
 PR 04-DEC-2003; 2003WO-EP050943.
 PR 02-FEB-2004; 2004WO-EP050067.
 PR 13-FEB-2004; 2004WO-EP050127.
 PR 19-MAR-2004; 2004WO-EP050334.
 PR 07-APR-2004; 2004WO-EP050464.
 PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX
 XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudmit J;

XX WPI; 2005-142879/15.
 DR N-PSDB; ADX01814.
 XX
 PT New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX
 PS Example 3; SEQ ID NO 71; 633pp; English.
 XX
 CC The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus scFv.
 XX
 SQ Sequence 244 AA;
 Query Match 100.0%; Score 576; DB 9; Length 244;
 Best Local Similarity 100.0%; Pred. No. 7e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYGNRPSPGIDPRF 60
 Db |||||
 134 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYGNRPSPGIDPRF 193
 Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
 Db |||||
 194 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 244
 XX
 RESULT 8
 ADW90312
 ID ADW90312 standard; protein; 247 AA.
 XX
 AC ADW90312;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Phage scFv SARS antibody SEQ ID NO 582.
 XX
 KW Virucide; Vaccine; diagnosis; Severe acute respiratory syndrome;
 KW respiratory-gen.; infection; respiratory disease; antibody.
 XX
 OS SARS coronavirus.
 XX
 PN WO2005012337-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 15-JUL-2004; 2004WO-EP051498.
 XX
 PR 15-JUL-2003; 2003WO-EP050308.
 PR 24-JUL-2003; 2003WO-EP050333.
 PR 02-SEP-2003; 2003WO-EP050392.
 PR 27-OCT-2003; 2003WO-EP050761.
 PR 24-NOV-2003; 2003WO-EP050863.
 XX
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Ter Meulen JH, Goudsmit J, Slootstra JW, Timmerman P, De Kruif CA;
 PI Van Den Brink EN;
 XX
 DR WPI; 2005-162947/17.
 XX
 XX New antigenic peptides from severe acute respiratory syndrome-coronavirus
 PT (SARS-CoV), useful in preparing a composition for diagnosing, treating or
 PT preventing SARS-CoV infection.
 XX
 PS Example 2; SEQ ID NO 582; 199pp; English.
 XX

CC The invention relates to an antigenic peptide from severe acute
 CC respiratory syndrome-coronavirus (SARS-CoV). The peptide or nucleic acid
 CC molecule encoding the peptide, fusion protein, conjugate or antibody is
 CC useful in preparing a composition for diagnosing, treating or preventing
 CC SARS-CoV infection. The present sequence represents a phage scFv SARS
 CC antibody.
 XX
 SQ Sequence 247 AA;
 Query Match 100.0%; Score 576; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 7.1e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYGNRPSPGIDPRF 60
 Db |||||
 137 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWYQKPGQAPVLVIYGNRPSPGIDPRF 196
 Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 111
 Db |||||
 197 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLGAAA 247
 XX
 RESULT 9
 ADX01809
 ID ADX01809 standard; protein; 247 AA.
 XX
 AC ADX01809;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE SARS coronavirus scFv antibody SEQ ID NO 65.
 XX
 KW Severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody.
 XX
 OS SARS coronavirus.
 XX
 PN WO2005012360-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 21-JUL-2004; 2004WO-EP051568.
 XX
 PR 22-JUL-2003; 2003WO-EP050328.
 PR 01-SEP-2003; 2003WO-EP050391.
 PR 16-OCT-2003; 2003WO-EP050723.
 PR 24-NOV-2003; 2003WO-EP050883.
 PR 04-DEC-2003; 2003WO-EP050943.
 PR 02-FEB-2004; 2004WO-EP050067.
 PR 13-FEB-2004; 2004WO-EP050127.
 PR 19-MAR-2004; 2004WO-EP050334.
 PR 07-APR-2004; 2004WO-EP050464.
 PR 14-APR-2004; 2004WO-EP050516.
 PR 29-APR-2004; 2004WO-EP050643.
 XX
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
 PI N-PSDB; ADX01808.
 XX
 DR WPI; 2005-142879/15.
 XX
 DR N-PSDB; ADX01808.
 XX
 PT New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.
 XX
 PS Example 3; SEQ ID NO 65; 633pp; English.
 XX
 CC The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunoconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a

CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus scFv.
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 576; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 7.1e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRRSPGIDPRF 60
 |||||
 DB 137 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRRSPGIDPRF 196
 |||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 111
 |||||
 DB 197 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 247
 |||||

RESULT 10
 ADR23324

ID ADR23324 standard; protein; 249 AA.
 XX
 AC ADR23324;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human CD72-targeted scFv Sc02-025.
 XX
 KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.
 XX
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Region 101..112
 FT /label= CDR3

PN WO2004067569-A1.
 XX
 PD 12-AUG-2004.
 XX
 PF 27-JAN-2003; 2003WO-EP050004.
 XX
 PR 27-JAN-2003; 2003WO-EP050004.
 XX
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX
 PI Bakker ABH, Marissen WE;
 XX
 PP WPI; 2004-580978/56.
 DR
 DR N-PSDB; ADR23323.
 XX

FT New internalizing human binding molecules capable of specifically binding
 FT to CD72, useful for diagnosing and/or treating B-cell associated
 FT diseases, such as cancer or autoimmune disorders.
 PT
 PS Example 3; SEQ ID NO 16; 174pp; English.
 XX

CC The present sequence is the protein sequence of Sc02-025, an scFv that
 CC specifically recognises human B cell associated antigen CD72. It
 CC comprises Vh1 Dp07 and Vh111 germline sequences. The scFv was selected
 CC from an antibody phage display library using human tonsillar mononuclear
 CC cells as target. It was shown to selectively bind to peripheral blood
 CC CD19+ B cells and to CD72-transfected L929 cells. Plasmid DNA was
 CC obtained from the scFv clone and used to determine the scFv nucleic acid
 CC and amino acid sequences. Sc02-025 scFv was used to generate CD72-
 CC directed human IgG1 antibodies comprising heavy chain ADR23350 and light
 CC chain ADR23362 sequences. Such anti-CD72 immunoglobulins or their antigen
 CC-binding fragments can be used as internalising human binding molecules
 CC of the invention. These internalising human binding molecules are capable
 CC of (specifically) binding to CD72 or its antigenic determinant, and
 CC preferably bind to CD72 associated with cells. Upon binding to CD72
 CC present on the surface of target cells, the binding molecules

CC internalise. In addition to the internalising human binding molecules,
 CC the invention provides immunoconjugates comprising an internalising human
 CC binding molecule and a tag (toxic substance, radioactive substance,
 CC liposome and/or enzyme), nucleic acids encoding these, and compositions
 CC comprising them. The internalising human binding molecule,
 CC immunoconjugate, nucleic acid molecule or composition can be used in the
 CC diagnosis and/or treatment of a B cell associated disorder or disease,
 CC especially a B cell associated cancer and B cell associated autoimmune
 CC disorder (claimed).
 XX
 SQ Sequence 249 AA;

Query Match 100.0%; Score 576; DB 8; Length 249;
 Best Local Similarity 100.0%; Pred. No. 7.1e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRRSPGIDPRF 60
 |||||
 DB 139 SELTQDPVAVSVALGQTVRITTCQGDLSRSYASWYQKPGQAPVLVIYGNRRSPGIDPRF 198
 |||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 111
 |||||
 DB 199 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFVGGTGLTVLGAAA 249
 |||||

RESULT 11
 ABG92023

ID ABG92023 standard; protein; 260 AA.
 XX
 AC ABG92023;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Antibody protein #3.
 XX
 KW Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 OS Unidentified.
 XX
 PN WO200253700-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 31-DEC-2001; 2001WO-US049442.
 XX
 PR 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX

(BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX
 PP WPI; 2002-674776/72.
 DR

XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX
 PS Disclosure; Fig 49; Opp; English.
 XX

CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 XX
 SQ Sequence 260 AA;

Query Match 100.0%; Score 576; DB 5; Length 260;
 Best Local Similarity 100.0%; Pred. No. 7.4e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPANVSVALGQTVRITTCQGSLSYSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 136 SELTQDPANVSVALGQTVRITTCQGSLSYSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 195
 QY 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
 DB 196 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 246

RESULT 12
 ABG92024
 ID ABG92024 standard; protein; 263 AA.
 XX
 AC ABG92024;

XX 04-DEC-2002 (first entry)
 XX Antibody protein #4.
 XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX Unidentified.
 XX WO200253700-A2.
 XX 11-JUL-2002.
 XX 31-DEC-2001; 2001WO-US049442.
 XX 29-DEC-2000; 2000US-00751181.
 XX 29-DEC-2000; 2000US-0258948P.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX Disclosure; Fig 50; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and

CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 XX
 SQ Sequence 263 AA;

Query Match 100.0%; Score 576; DB 5; Length 263;
 Best Local Similarity 100.0%; Pred. No. 7.5e-35;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPANVSVALGQTVRITTCQGSLSYSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
 DB 133 SELTQDPANVSVALGQTVRITTCQGSLSYSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 192
 QY 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
 DB 193 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 243

RESULT 13
 ABG92020
 ID ABG92020 standard; protein; 266 AA.
 XX
 AC ABG92020;

XX 04-DEC-2002 (first entry)
 XX Human antibody fragment #204.
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX Homo sapiens.

XX WO200253700-A2.
 XX 11-JUL-2002.
 XX 31-DEC-2001; 2001WO-US049442.
 XX 29-DEC-2000; 2000US-00751181.
 XX 29-DEC-2000; 2000US-0258948P.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

XX PS Disclosure; Page 309-310; Opp; English.

XX CC The invention relates to an isolated epitope present on cancer cells and

XX CC important in physiological phenomena such as cell rolling, metastasis and

XX CC inflammation, where the epitope is capable of being bound by an antibody,

XX CC its antigen-binding fragment or its complex comprising at least one

XX CC antibody or its binding fragment having a first hypervariable region. The

XX CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

XX CC disease, thrombosis, restenosis, metastasis, growth and/or replication of

XX CC tumour or leukaemia cells, increase in number of tumour or leukaemia

XX CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

XX CC platelet and/or cell-platelet adhesion or aggregation, for increasing

XX CC mortality of tumour or leukaemia cells, for increasing the susceptibility

XX CC of diseased cells to damage by anti-disease, anti-cancer or anti-

XX CC leukaemia agents, or for decreasing the number of tumour or leukaemia

XX CC cells in a patient, or in the manufacture of a medicament for the above

XX CC mentioned purposes. The epitopes are useful for diagnosing and treating

XX CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory

XX CC diseases, cardiovascular diseases such as myocardial infarction,

XX CC retinopathic diseases and other diseases mediated by abnormal platelet

XX CC function and diseases caused by sulphated tyrosine-dependent protein-

XX CC protein interactions. This sequence represents a human antibody fragment

XX CC of the invention

XX SQ Sequence 266 AA;

Query Match 100.0%; Score 576; DB 5; Length 266;

Best Local Similarity 100.0%; Pred. No. 7.6e-35;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60

DB 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQDEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111

DB 213 SGSSSGNTASLTITGAQDEADYYCNSRDSGNHVVFGGTKLTVLGAAA 263

RESULT 14

ABG78150

ID ABG78150 standard; protein; 277 AA.

XX AC ABG78150;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #25.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

XX PT

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

XX Claim 4; Page 155-156; 232pp; English.

XX CC The invention relates to a peptide or polypeptide comprising an Fv

XX CC molecule, a construct or fragments or a construct of a fragment with

XX CC enhanced binding characteristics which selectively and/or specifically

XX CC binds to a target cell in favour of other cells, where binding is

XX CC primarily determined by a first hypervariable region and Fv is a single

XX CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX CC association with or attached, coupled, combined, linked or fused to a

XX CC pharmaceutical agent, is useful in the manufacture of a medicament, where

XX CC the medicament has activity against a diseased cell, preferably a cancer

XX CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

XX CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

XX CC acute myeloid leukaemia cell). The peptide is also useful for preparing a

XX CC composition for use in inhibiting the growth of a diseased or cancer

XX CC cell. This sequence represents a human Fv molecule hypervariable region

XX CC related peptide of the invention

XX SQ Sequence 277 AA;

Query Match 100.0%; Score 576; DB 5; Length 277;

Best Local Similarity 100.0%; Pred. No. 7.9e-35;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 60

DB 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQDEADYYCNSRDSGNHVVFGGTKLTVLGAAA 111

DB 213 SGSSSGNTASLTITGAQDEADYYCNSRDSGNHVVFGGTKLTVLGAAA 263

RESULT 15

ABG78328

ID ABG78328 standard; protein; 277 AA.

XX AC ABG78328;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #203.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plaksin D, Peretz T;

XX DR WPI; 2002-619166/66.

XX DR N-PSDB; ABS63384.

XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX PT cells.

PS Claim 141; Fig 14; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (FcFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention

XX Sequence 277 AA;

Query Match 100.0%; Score 576; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.9e-35;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPNVSVALGQTVRITCGDSLSRSYYASWYQKPGQAPVLVIYKNNRPSGIPDRF 60
Db 153 SELTQDPNVSVALGQTVRITCGDSLSRSYYASWYQKPGQAPVLVIYKNNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNNHVFVGGGKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSGNNHVFVGGGKLTVLGAAA 263

Search completed: November 18, 2005, 21:46:15
Job time : 64.6278 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:40:23 ; Search time 15.2319 Seconds
(without alignments)
602.487 Million cell updates/sec

Title: US-10-029-926D-7
Perfect score: 576
Sequence: 1 SELTQDPAVSVALGQTVRIT.....SGNHVFGGKTLTVLGAAA 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	576	100.0	278	2	US-09-260-527-3
2	576	100.0	280	2	US-09-260-527-1
3	576	100.0	309	2	US-09-079-029-9
4	576	100.0	312	2	US-09-079-029-10
5	558	96.9	108	2	US-09-720-493-4
6	554	96.2	111	2	US-09-203-768A-8
7	537	93.2	109	1	US-08-632-816A-16
8	531.5	92.3	109	1	US-08-665-202-34
9	531.5	92.3	109	2	US-09-315-574-34
10	525	91.1	101	2	US-09-726-219A-168
11	525	91.1	101	2	US-09-196-522-168
12	502	87.2	97	1	US-08-665-202-35
13	502	87.2	97	2	US-08-315-574-35
14	494.5	85.9	104	2	US-08-793-450-2
15	494.5	85.9	238	2	US-08-793-450-6
16	487	84.5	104	2	US-09-240-274-49
17	487	84.5	104	2	US-09-848-798-49
18	480	83.3	106	2	US-09-240-274-48
19	480	83.3	106	2	US-08-848-798-48
20	475.5	82.6	102	2	US-09-726-219A-174
21	475.5	82.6	102	2	US-09-196-522-174
22	473	82.1	106	2	US-09-240-274-47
23	473	82.1	106	2	US-09-240-274-50
24	473	82.1	106	2	US-09-848-798-47
25	473	82.1	106	2	US-09-848-798-50
26	471	81.8	103	1	US-08-273-146-71
27	448.5	77.9	108	2	US-09-025-769B-20

28	448.5	77.9	108	2	US-09-490-070A-20
29	448.5	77.9	108	2	US-09-490-153-20
30	448.5	77.9	108	2	US-09-490-324-20
31	443.5	77.0	105	1	US-08-488-113B-157
32	443.5	77.0	105	1	US-08-477-484B-157
33	443.5	77.0	105	1	US-08-107-669D-21
34	443.5	77.0	105	1	US-08-472-788A-21
35	443.5	77.0	105	1	US-08-477-531B-21
36	443.5	77.0	105	1	US-08-646-360-157
37	443.5	77.0	105	1	US-08-082-842A-21
38	443.5	77.0	105	2	US-08-839-765-157
39	443.5	77.0	105	2	US-09-136-389-157
40	443.5	77.0	105	2	US-09-610-838-157
41	443.5	77.0	105	2	US-09-711-485-157
42	441	76.6	125	2	US-09-471-276-1249
43	423	73.4	108	1	US-08-360-125-12
44	423	73.4	108	1	US-08-450-578-12
45	423	73.4	108	1	US-09-017-628-12

ALIGNMENTS

RESULT 1

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match 100.0%; Score 576; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SELTQDPAVSVALGQTVRITCCGDSLSYSYASVYQQKPGQAPVLIYGNRPSGIPDRF 60
Db	154	SELTQDPAVSVALGQTVRITCCGDSLSYSYASVYQQKPGQAPVLIYGNRPSGIPDRF 213
Qy	61	SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGKTLTVLGAAA 111
Db	214	SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGKTLTVLGAAA 264

RESULT 2

US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26


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/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 280
/ TYPE: PRT
/ ORGANISM: UNKNOWN
/ FEATURE:
/ OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
/ OTHER INFORMATION: phage display library known as the Synthetic scFv
/ OTHER INFORMATION: Library (#1) from the Centre for Protein
/ OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match      100.0%; Score 576; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 156 SELTQDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 215

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVVFGGTTKLTVLGAAA 111
Db 216 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVVFGGTTKLTVLGAAA 266

RESULT 3
US-09-079-029-9
/ Sequence 9, Application US/09079029
/ Patent No. 6342369
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camilla W.
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Chuntharapai, Anan
/ APPLICANT: Kim, Kyung J.
/ TITLE OF INVENTION: Apo-2 Receptor
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/079,029
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marschang, Diane L.
/ REGISTRATION NUMBER: 35,600
/ REFERENCE/DOCKET NUMBER: P1101R2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5416
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 309 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
US-09-079-029-9

Query Match      100.0%; Score 576; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
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Db 176 SELTQDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 235
QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVVFGGTTKLTVLGAAA 111
Db 236 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVVFGGTTKLTVLGAAA 286

RESULT 4
US-09-079-029-10
/ Sequence 10, Application US/09079029
/ Patent No. 6342369
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camilla W.
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Chuntharapai, Anan
/ APPLICANT: Kim, Kyung J.
/ TITLE OF INVENTION: Apo-2 Receptor
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/079,029
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marschang, Diane L.
/ REGISTRATION NUMBER: 35,600
/ REFERENCE/DOCKET NUMBER: P1101R2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5416
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 312 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
US-09-079-029-10

Query Match      100.0%; Score 576; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.8e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 179 SELTQDPAVSVAGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 238

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVVFGGTTKLTVLGAAA 111
Db 239 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVVFGGTTKLTVLGAAA 289

RESULT 5
US-09-720-493-4
/ Sequence 4, Application US/09720493
/ Patent No. 6827925
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Williams, Andrew J
/ APPLICANT: Tempest, Philip R
/ APPLICANT: Holtet, Thor L
/ APPLICANT: Main, Sarah H
/ APPLICANT: Jackson, Helen
/ APPLICANT: Daramola, Olalekan
```

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; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHE/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-720-493-4

Query Match          96.9%; Score 558; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.8e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPVAVSVALGQTVRITTCQGSLSRSYYASWYQQKPGAPLVLYGKNNRPSGIPDRF 60
Db 2 SELTQDPVAVSVALGQTVRITTCQGSLSRSYYASWYQQKPGAPLVLYGKNNRPSGIPDRF 61

Qy 61 SGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHVVFGGTKLTVL 107
Db 62 SGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHVVFGGTKLTVL 108

RESULT 6
US-09-203-768A-8
; Sequence 8, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-8

Query Match          96.2%; Score 554; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 7e-46;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SELTQDPVAVSVALGQTVRITTCQGSLSRSYYASWYQQKPGAPLVLYGKNNRPSGIPDRF 60
Db 2 SELTQDPVAVSVALGQTVRITTCQGSLSRSYYASWYQQKPGAPLVLYGKNNRPSGIPDRF 61

Qy 61 SGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHVVFGGTKLTVLG 108
Db 62 SGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHVVFGGTKLTVLG 109

RESULT 7
US-08-652-816A-16
; Sequence 16, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHE/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-720-493-4

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-16

Query Match          93.2%; Score 537; DB 1; Length 109;
Best Local Similarity 96.2%; Pred. No. 2.9e-44;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SELTQDPVAVSVALGQTVRITTCQGSLSRSYYASWYQQKPGAPLVLYGKNNRPSGIPDRF 60
Db 2 SELTQDPVAVSVALGQTVRITTCQGSLSRSYYASWYQQKPGAPLVLYGKNNRPSGIPDRF 61

Qy 61 SGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHVVFGGTKLTV 106
Db 62 SGSSSGNTASLTITGAQAEDADYYCNSRDSGNNHVVFGGTKLEI 107

RESULT 8
US-08-665-202-34
; Sequence 34, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-665-202-34

Query Match 92.3%; Score 531.5; DB 1; Length 109;
Best Local Similarity 95.4%; Pred. No. 9.8e-44;
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVVFGGGKTLVLG 108
Db 61 SGSSSGNIASLTITGAQAEADYYCNSRDSSGNPYWVFGGKTVVLG 109

RESULT 9
US-09-315-574-34
; Sequence 34, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-34

Query Match 92.3%; Score 531.5; DB 2; Length 109;
Best Local Similarity 95.4%; Pred. No. 9.8e-44;
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVVFGGGKTLVLG 108
Db 61 SGSSSGNIASLTITGAQAEADYYCNSRDSSGNPYWVFGGKTVVLG 109

RESULT 10
US-09-726-219A-168
; Sequence 168, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Grifiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12

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; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-168

Query Match          91.1%; Score 525; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.7e-43;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPASVALGQTVRIITCGDSLRSYASWYQKFGQAPVLVIYKNNRPSGIPDRF 60
   |||||||
Db 2 SELTQDPASVALGQTVRIITCGDSLRSYASWYQKFGQAPVLVIYKNNRPSGIPDRF 61
   |||||||

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 100
   |||||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 101
   |||||||

RESULT 11
US-09-196-522-168
; Sequence 168, Application US/09196522
; Patent No. 6316605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-168

Query Match          91.1%; Score 525; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.7e-43;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPASVALGQTVRIITCGDSLRSYASWYQKFGQAPVLVIYKNNRPSGIPDRF 60
   |||||||
Db 2 SELTQDPASVALGQTVRIITCGDSLRSYASWYQKFGQAPVLVIYKNNRPSGIPDRF 61
   |||||||

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 100
   |||||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGG 101
   |||||||

RESULT 12
US-08-665-202-35
; Sequence 35, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-35

Query Match          87.2%; Score 502; DB 1; Length 97;
Best Local Similarity 99.0%; Pred. No. 5.7e-41;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 SELTQDPAVSVALGQTVRITTCQDLSRYSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Db 1 SSSLTQDPAVSVALGQTVRITTCQDLSRYSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Qy 61 SGSSSGNTASLITITGAQAEADYYCNSRDSSGNHVV 97
 Db 61 SGSSSGNTASLITITGAQAEADYYCNSRDSSGNHVV 97

RESULT 13

US-09-315-574-35
 ; Sequence 35, Application US/09315574
 ; Patent No. 6512097
 ; GENERAL INFORMATION:
 ; APPLICANT: Marks, James D.
 ; APPLICANT: Schier, Robert
 ; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
 ; TITLE OF INVENTION: Tumor Antigens
 ; NUMBER OF SEQUENCES: 141
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4106
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/315,574
 ; FILING DATE: 20-MAY-99
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,238
 ; FILING DATE: 14-JUN-1995
 ; APPLICATION DATA:
 ; FILING DATE: 15-JUN-1995
 ; APPLICATION NUMBER: US 08/665,202
 ; FILING DATE: 13-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom
 ; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 02307E-061411
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 97 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-315-574-35

Query Match 87.2%; Score 502; DB 2; Length 97;
 Best Local Similarity 99.0%; Pred. No. 5.7e-41;
 Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SELTQDPAVSVALGQTVRITTCQDLSRYSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Db 1 SSSLTQDPAVSVALGQTVRITTCQDLSRYSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 60
 Qy 61 SGSSSGNTASLITITGAQAEADYYCNSRDSSGNHVV 97
 Db 61 SGSSSGNTASLITITGAQAEADYYCNSRDSSGNHVV 97

RESULT 14

US-08-793-450-2
 ; Sequence 2, Application US/08793450
 ; Patent No. 6312690
 ; GENERAL INFORMATION:
 ; APPLICANT: EDELMAN, LENA
 ; APPLICANT: MARGARITTE, CHRISTEL
 ; APPLICANT: KACZOREK, MICHEL
 ; APPLICANT: CHAABIHI, HASSAN
 ; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,450
 ; FILING DATE: 03-MAR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 94/10566
 ; FILING DATE: 02-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 104 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-793-450-2

Query Match 85.9%; Score 494.5; DB 2; Length 104;
 Best Local Similarity 90.7%; Pred. No. 3.2e-40;
 Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;
 Qy 2 ELTQDPAVSVALGQTVRITTCQDLSRYSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 61
 Db 3 ELTQDPAVSVALGQTVRITTCQDLSRYSYASWYQKPGQAPVLVIYGNRRPSGIDPRF 62
 Qy 62 GSSSGNTASLITITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 108
 Db 63 GSSSGNTASLITITGAQAEADYYCNSGGK-----VFGGTKLTVLG 104

RESULT 15

US-08-793-450-6
 ; Sequence 6, Application US/08793450
 ; Patent No. 6312690
 ; GENERAL INFORMATION:
 ; APPLICANT: EDELMAN, LENA
 ; APPLICANT: MARGARITTE, CHRISTEL
 ; APPLICANT: KACZOREK, MICHEL
 ; APPLICANT: CHAABIHI, HASSAN
 ; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,450
 ; FILING DATE: 03-MAR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 94/10566
 ; FILING DATE: 02-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 680-118-0 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 238 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-793-450-6

Query Match 85.9%; Score 494.5, DB 2; Length 238;
 Best Local Similarity 90.7%; Pred. No. 8.3e-40;
 Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;
 Qy 2 ELTQDPVSVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSPGIPDRFS 61
 Db |||||
 Qy 22 ELTQDPVSVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSPGIPDRFS 81
 Db |||||
 Qy 62 GSSSGNTASLTITGAQAEDEADYYCNSRDSNGHVFGGGTKLTVLG 108
 Db |||||
 Qy 82 GSSSGNTASLTITGAQAEDEADYYCNSRDSNGHVFGGGTKLTVLG 123
 Db |||||

Search completed: November 18, 2005, 21:55:04
 Job time : 17.2319 secs

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Result No.	Score	Query Match	CONTROLS			Description
			Length	DB	ID	
1	576	100.0	111	15	US-10-032-037B-7	Sequence 7, Appli
2	576	100.0	111	15	US-10-029-988B-7	Sequence 7, Appli
3	576	100.0	111	15	US-10-032-423A-7	Sequence 7, Appli
4	576	100.0	111	15	US-10-029-326B-7	Sequence 7, Appli
5	576	100.0	125	17	US-10-888-959-8	Sequence 8, Appli
6	576	100.0	266	15	US-10-032-037B-204	Sequence 204, App
7	576	100.0	266	15	US-10-029-988B-204	Sequence 204, App
8	576	100.0	266	15	US-10-032-423A-204	Sequence 204, App
9	576	100.0	277	15	US-10-032-037B-25	Sequence 25, Appl
10	576	100.0	277	15	US-10-032-037B-203	Sequence 203, App
11	576	100.0	277	15	US-10-029-988B-25	Sequence 25, Appl
12	576	100.0	277	15	US-10-029-988B-203	Sequence 203, App
13	576	100.0	277	15	US-10-032-423A-25	Sequence 25, Appl

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; Sequence 7, Application US/10029988B
; Publication No. US20040001833A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-7

Query Match      100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 3
US-10-032-423A-7
; Sequence 7, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-7

Query Match      100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 4
US-10-029-926B-7
; Sequence 7, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
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; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-7

Query Match      100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 5
US-10-888-959-8
; Sequence 8, Application US/10888959
; Publication No. US20050048545A1
; GENERAL INFORMATION:
; APPLICANT: Cull, Millard
; APPLICANT: Brennan, Miles
; APPLICANT: Gill, Ronald
; TITLE OF INVENTION: Universal Detection of Binding
; FILE REFERENCE: BPP 03
; CURRENT APPLICATION NUMBER: US/10/888,959
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/487,018
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/509,196
; PRIOR FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variable light chain domain
US-10-888-959-8

Query Match      100.0%; Score 576; DB 17; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 1 SELTQDPAVSVALGQTVRITTCQGDLSRSYASMTYQKPGQAPVLVIYKKNRPSGIPDRF 60

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTTKLTVLGAAA 111

RESULT 6
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US2004001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
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; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032.037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match 100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 263

RESULT 7

US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029.988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 263

RESULT 8

US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032.423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000

; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match 100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 263

RESULT 9

US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032.037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match 100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPAVSVAGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 263

RESULT 10

US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032.037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT

; ORGANISM: Homo sapiens
 US-10-032-037B-203

Query Match 100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; -Pred. NO. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0

Qy	1	SELTQDP	AVS	VAL	G	T	R	I	T	C	G	D	S	L	R	S	Y	A	S	W	Y	Q	K	P	G	Q	A	P	V	L	V	I	Y	K	N	R	P	S	G	I	P	D	R	F	60
Db	153	SELTQDP	AVS	VAL	G	T	R	I	T	C	G	D	S	L	R	S <td>Y</td> <td>A</td> <td>S</td> <td>W</td> <td>Y</td> <td>Q</td> <td>K</td> <td>P</td> <td>G</td> <td>Q</td> <td>A</td> <td>P</td> <td>V</td> <td>L</td> <td>V</td> <td>I</td> <td>Y</td> <td>K <td>N</td> <td>R</td> <td>P</td> <td>S</td> <td>G</td> <td>I</td> <td>P</td> <td>D</td> <td>R</td> <td>F</td> <td>212</td> </td>	Y	A	S	W	Y	Q	K	P	G	Q	A	P	V	L	V	I	Y	K <td>N</td> <td>R</td> <td>P</td> <td>S</td> <td>G</td> <td>I</td> <td>P</td> <td>D</td> <td>R</td> <td>F</td> <td>212</td>	N	R	P	S	G	I	P	D	R	F	212

[illegible]

```

RESULT 11
US-10-029-988B-25
/ Sequence 25, Application US/10029988B
/ Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ TITLE OF INVENTION: MOJETTES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-988B-25

```

Qy	1	SELTQDPAVSVALGQTVRTTCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIDRF	60
	153	SELTQDPAVSVALGQTVRTTCQDLSRSYYASWYQKPGQAPVLVIYGNRPSGIDRF	212

Qy 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGTKITVLGAAA 111
|||
Db 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGTKITVLGAAA 263

```

RESULT 12
US-10-029-988B-203
/ Sequence 203, Application US/10029988B
/ Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 203
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-988B-203

```

	Matches	111;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	SELTQDPAVSVALGQTVRITCGSDLSURSYYASWYQKPGQAPVLVIYIGKNRSGIPDRF	60							
Db	153	SELTQDPAVSVALGQTVRITCGSDLSURSYYASWYQKPGQAPVLVIYIGKNRSGIPDRF	212							
Qy	61	SGSSSGNTASLTITGCAADEADYYCNSRDSGNNHVFGGTXLTVLGA	111							
Db	213	SGSSSGNTASLTITGCAADEADYYCNSRDSGNNHVFGGTXLTVLGA	263							

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RESULT 13
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-25

```

Qy	1	SELTQDP	PAVS	VAL	QGT	VR	IT	COG	SL	RS	YY	AS	WY	QK	PG	AP	PVL	VI	YK	NR	PS	GI	DR	60
D6	153	SELTQDP	PAVS	VAL	QGT <td>VR</td> <td>IT <td>COG</td> <td>SL <td>RS <td>YY <td>AS <td>WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td></td></td></td></td></td></td>	VR	IT <td>COG</td> <td>SL <td>RS <td>YY <td>AS <td>WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td></td></td></td></td></td>	COG	SL <td>RS <td>YY <td>AS <td>WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td></td></td></td></td>	RS <td>YY <td>AS <td>WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td></td></td></td>	YY <td>AS <td>WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td></td></td>	AS <td>WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td></td>	WY <td>QK</td> <td>PG</td> <td>AP</td> <td>PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td></td>	QK	PG	AP	PVL <td>VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td></td>	VI <td>YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td></td>	YK <td>NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td></td>	NR <td>PS <td>GI <td>DR</td> <td>212</td> </td></td>	PS <td>GI <td>DR</td> <td>212</td> </td>	GI <td>DR</td> <td>212</td>	DR	212

QY	61	SGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHVFGGKTTLVLGAAA	111
D6	213	SGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHVFGGKTTLVLGAAA	263

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RESULT 14
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203

```

[illegible]

Qy 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 263

RESULT 15

US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/23/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match 100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCQDLSLSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 60
Db 153 SELTQDPAVSVALGQTVRITCQDLSLSYASWYQKPGQAPVLVIYKKNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYCNRSRDSGNHVVFGGTKLTVLGAAA 263

Search completed: April 25, 2005, 21:09:46
Job time : 50.1009 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:47:37 ; Search time 49.3722 Seconds
(without alignments)
939.375 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576

Sequence: 1 SELTQDPAVSVALGQTVRIT.....SGNHVFGGTKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pdb:

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pdb:

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pdb:

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pdb:

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pdb:

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	4	US-10-032-037B-7
2	576	100.0	111	4	US-10-029-988B-7
3	576	100.0	111	4	US-10-032-423A-7
4	576	100.0	111	4	US-10-029-926B-7
5	576	100.0	112	6	US-11-039-767-18
6	576	100.0	125	5	US-10-888-959-8
7	576	100.0	266	4	US-10-032-037B-204
8	576	100.0	266	4	US-10-029-988B-204
9	576	100.0	266	4	US-10-032-423A-204
10	576	100.0	277	4	US-10-032-037B-25
11	576	100.0	277	4	US-10-032-037B-203
12	576	100.0	277	4	US-10-029-988B-25
13	576	100.0	277	4	US-10-029-988B-203
14	576	100.0	277	4	US-10-032-423A-25
15	576	100.0	277	4	US-10-032-423A-203
16	576	100.0	277	4	US-10-029-926B-25
17	576	100.0	277	4	US-10-029-926B-203
18	576	100.0	277	4	US-10-610-843B-1
19	576	100.0	278	4	US-10-610-843B-2
20	576	100.0	280	4	US-10-610-843B-3
21	576	100.0	280	4	US-10-611-588C-1
22	576	100.0	280	5	US-10-880-922-5
23	576	100.0	280	5	US-10-880-922-6
24	576	100.0	280	5	US-10-880-922-55
25	576	100.0	280	5	US-10-880-922-56
26	576	100.0	280	5	US-10-880-922-60
27	576	100.0	280	5	US-10-880-922-61

28	576	100.0	309	4	US-10-052-798-9	Sequence 9, Appli
29	576	100.0	309	4	US-10-288-917-9	Sequence 9, Appli
30	576	100.0	309	4	US-10-423-448-9	Sequence 9, Appli
31	576	100.0	312	4	US-10-052-798-10	Sequence 10, Appli
32	576	100.0	312	4	US-10-288-917-10	Sequence 10, Appli
33	576	100.0	312	4	US-10-423-448-10	Sequence 10, Appli
34	568	98.6	110	4	US-10-800-197-115	Sequence 115, App
35	568	98.6	110	4	US-10-800-197-119	Sequence 119, App
36	564	97.9	153	3	US-09-988-115A-59	Sequence 59, Appli
37	564	97.9	153	5	US-10-705-519-59	Sequence 59, Appli
38	564	97.9	237	3	US-09-880-748-1941	Sequence 1941, Ap
39	564	97.9	237	3	US-09-880-748-2112	Sequence 2112, Ap
40	564	97.9	237	4	US-10-293-418-1941	Sequence 1941, Ap
41	564	97.9	237	4	US-10-293-418-2112	Sequence 2112, Ap
42	564	97.9	238	3	US-09-880-748-1907	Sequence 1907, Ap
43	564	97.9	238	4	US-10-293-418-1907	Sequence 1907, Ap
44	564	97.9	238	6	US-11-090-847-81	Sequence 81, Appli
45	564	97.9	238	6	US-11-090-847-103	Sequence 103, App

ALIGNMENTS

RESULT 1

US-10-032-037B-7

Sequence 7, Application US/10032037B

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCES: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7

LENGTH: 111

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-037B-7

Query Match 100.0%; Score 576; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCCGDSLSRSYASVYQKPGQAPVLVIYKKNRPSGIDRPF 60

Db 1 SELTQDPAVSVALGQTVRITCCGDSLSRSYASVYQKPGQAPVLVIYKKNRPSGIDRPF 60

Qy 61 SGSSSGNTASLTITGAQAEADYDCNSRDSGNHVVFGGTKLTVLGAAA 111

Db 61 SGSSSGNTASLTITGAQAEADYDCNSRDSGNHVVFGGTKLTVLGAAA 111

RESULT 2

US-10-029-988B-7

Sequence 7, Application US/10029988B

Publication No. US20040001839A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCES: 10793/46

CURRENT APPLICATION NUMBER: US/10/029,988B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7


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; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-7

Query Match      100.0%; Score 576; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||

RESULT 3
US-10-032-423A-7
; Sequence 7, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-7

Query Match      100.0%; Score 576; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||

RESULT 4
US-10-029-926B-7
; Sequence 7, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-7

Query Match      100.0%; Score 576; DB 4; Length 111;
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Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||

RESULT 5
US-11-039-767-18
; Sequence 18, Application US/11039767
; Publication No. US20050170398A1
; GENERAL INFORMATION:
; APPLICANT: CRUCCELL HOLLAND B.V.
; TITLE OF INVENTION: Recombinant production of mixtures of antibodies
; FILE REFERENCE: 0079 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/039,767
; CURRENT FILING DATE: 2005-01-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: common VL sequence of clones B28 (anti-CD22 phase), II-2
; OTHER INFORMATION: (anti-CD72 phase) and I-2 (anti-class II phase)
US-11-039-767-18

Query Match      100.0%; Score 576; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
   |||||||
Db 2 SELTQDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 61
   |||||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 111
   |||||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGAAA 112
   |||||||

RESULT 6
US-10-888-959-8
; Sequence 8, Application US/10888959
; Publication No. US20050048545A1
; GENERAL INFORMATION:
; APPLICANT: Cull, Millard
; APPLICANT: Brennan, Miles
; APPLICANT: Gill, Ronald
; TITLE OF INVENTION: Universal Detection of Binding
; FILE REFERENCE: BPP-03
; CURRENT APPLICATION NUMBER: US/10/888,959
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/487,018
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/509,196
; PRIOR FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variable light chain domain
US-10-888-959-8

Query Match      100.0%; Score 576; DB 5; Length 125;
```

Best Local Similarity 100.0%; Pred. No. 4.6e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
|||||

Db 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
|||||

Qy 61 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 111
|||||

Db 61 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 111
|||||

RESULT 7

US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match 100.0%; Score 576; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
|||||

Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 111
|||||

Db 213 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 263
|||||

RESULT 8

US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match 100.0%; Score 576; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
|||||

Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 111
|||||

Db 213 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 263
|||||

RESULT 9

US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match 100.0%; Score 576; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
|||||

Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 111
|||||

Db 213 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 263
|||||

RESULT 10

US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match 100.0%; Score 576; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 60
|||||

Db 153 SELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYKNNRPSGIDPRF 212
|||||

Qy 61 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 111
|||||

Db 213 SGSSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGKTTLVLGAAA 263
|||||

```

RESULT 11
US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOETITIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032.037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-203

```

```

; Publication No. US20040001839A1
;
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-029-988B-203

```

	Query Match	100.0%	Score 576;	DB 4;	Length 277;
	Best Local Similarity	100.0%;	Pred. No. 1.1e-43;		
	Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SELTQDPAVSV	ALGQTVRITCGD	SLRSYYASWYQKPGQAPVLVIYKNNRP	SGIPDRF 60
Db	153	SELTQDPAVSV	ALGQTVRITCGD	SLRSYYASWYQKPGQAPVLVIYKNNRP	SGIPDRF 212
Qy	61	SGSSSGNTAS	LTITGAQAEAD	YYCNRSRDSGGNHVVF	GGTKLTVLGAAA 111
Db	213	SGSSSGNTAS	LTITGAQAEAD	YYCNRSRDSGGNHVVF	GGTKLTVLGAAA 263

```

Query Match      100.0%; Score 576; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  SELTQDPAVSVALGQTVRITTCQSDLSRSYASWYQKPGQAPVLVIYGNKRPSPGIDRF 60
Db      153 SELTQDPAVSVALGQTVRITTCQSDLSRSYASWYQKPGQAPVLVIYGNKRPSPGIDRF 212

Qy      61  SGSSSGNTASLTITTAQAEDADYYCNRSRDSGNHVVFGGGTKLTVLGAAA 111
Db      213 SGSSSGNTASLTITTAQAEDADYYCNRSRDSGNHVVFGGGTKLTVLGAAA 263

RESULT 15
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

```

FILE REFERENCE: 10793/45
CURRENT APPLICATION NUMBER: US/10/032,423A
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 203
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 100.0%; Score 576; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SELTQDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 60
Db 153 SELTQDPVAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRPSGIPDRF 212
Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVFGGTKLTVLGAAA 111
Db 213 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVFGGTKLTVLGAAA 263

Search completed: November 18, 2005, 22:17:51
Job time : 50.3722 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:53:49 ; Search time 1.40063 Seconds
(without alignments)
89.536 Million cell updates/sec

Title: US-10-029-926D-7

Perfect score: 5%

Sequence: 1 SELTQDPASVALGQTVRIT.....SGNHVFGGTKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	51.7	258	1	US-10-512-184-26
2	298	51.7	327	1	US-10-512-184-62
3	298	51.7	327	1	US-10-512-184-64
4	298	51.7	328	1	US-10-512-184-63
5	298	51.7	575	1	US-10-512-184-65
6	298	51.7	625	1	US-10-512-184-47
7	297.5	51.6	252	1	US-10-512-184-28
8	292	50.7	261	1	US-10-512-184-35
9	292	50.7	313	1	US-10-512-184-72
10	286	49.7	250	1	US-10-512-184-27
11	254	44.1	106	7	US-11-174-186-7
12	250.5	43.5	128	1	US-10-721-763-31
13	249	43.2	626	1	US-10-512-184-49
14	248.5	43.1	259	1	US-10-512-184-34
15	248.5	43.1	371	1	US-10-512-184-71
16	247.5	43.0	543	1	US-10-495-664-3
17	246.5	42.8	131	1	US-10-721-763-27
18	244	42.4	106	7	US-11-174-186-11
19	244	42.4	106	7	US-11-174-186-12
20	244	42.4	106	7	US-11-174-186-13
21	243	42.2	106	7	US-11-174-186-15
22	242	42.0	106	7	US-11-174-186-10
23	242	42.0	106	7	US-11-174-186-14
24	241.5	41.9	263	1	US-10-512-184-29
25	239	41.5	106	7	US-11-174-186-1

26	239	41.5	106	7	US-11-174-186-9	Sequence 9, Appli
27	239	41.5	106	7	US-11-174-186-16	Sequence 12, Appl
28	239	41.5	213	7	US-11-174-186-42	Sequence 46, Appl
29	238.5	41.4	129	1	US-10-721-763-19	Sequence 19, Appl
30	238	41.3	113	1	US-10-932-334-61	Sequence 7, Appli
31	236	41.0	109	1	US-10-726-554-7	Sequence 61, Appli
32	235	40.8	127	1	US-10-839-799-27	Sequence 27, Appli
33	234	40.6	106	7	US-11-174-186-8	Sequence 8, Appli
34	233.5	40.5	259	1	US-10-512-184-31	Sequence 31, Appl
35	233.5	40.5	329	1	US-10-512-184-68	Sequence 68, Appl
36	232	40.3	113	1	US-10-932-334-64	Sequence 64, Appl
37	231.5	40.2	110	1	US-10-648-816-2	Sequence 2, Appli
38	231.5	40.2	110	1	US-10-648-816-3	Sequence 3, Appli
39	231.5	40.2	110	1	US-10-648-816-4	Sequence 4, Appli
40	231.5	40.2	110	1	US-10-648-816-5	Sequence 6, Appli
41	231.5	40.2	110	1	US-10-648-816-7	Sequence 7, Appli
42	231.5	40.2	110	1	US-10-648-816-8	Sequence 8, Appli
43	231.5	40.2	126	1	US-10-839-799-75	Sequence 75, Appli
44	231.5	40.2	129	1	US-10-721-763-23	Sequence 23, Appl
45	231	40.1	112	7	US-11-012-353-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1

US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv CWP2
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-26

Query Match 51.7%; Score 298; DB 1; Length 258;
Best Local Similarity 59.5%; Pred No. 2.2e-16;
Matches 66; Conservative 10; Mismatches 27; Indels 8; Gaps 4;
Qy 3 LTQDPASVALGQTVRITCGDSLRSYASWYQOK-PQAPVLVIYGN---NRPSGIPD 58
Db 149 LTQPSSVSANLGGTVEITCSG---GYRCWFQKSPGAPVTVIYDDDSANRPSNIPS 205
Qy 59 RPSGSSGNTASLTITCAQAEDEADYYCNSRDSSGNHV-VFGGTKLTVLG 108
Db 206 RPSGSGSTATLTITGVQADDEAVYFCGSDYDRSSGYVSIFGAGTTLTVLG 256

RESULT 2

US-10-512-184-62
; Sequence 62, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184


```

; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFv CWP2 - cmcy/H186.
US-10-512-184-47

Query Match          51.7%; Score 298; DB 1; Length 625;
Best Local Similarity 59.5%; Pred. No. 4.5e-16;
Matches 66; Conservative 10; Mismatches 27; Indels 8; Gaps 4;

QY 3 LTQDPVSVVALGQTVRTITCGDLSLSYASWYQOK-PQAPVLVIYGN---NRPSGIPD 58
.Db 490 LTPSSVSANLGTVEITCGSG--GYRYGWFQKSPGAPVTVIYWDSDSANRPSNIPS 546
;
QY 59 FSGSSGNTASLTITGAQAEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
.Db 547 FSGSTSGTATLTITGVQADDEAVYFCGSDYRSGYVSIFGAGTTLTVLG 597
;

RESULT 7
US-10-512-184-28
; Sequence 28, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv FPCWPA5
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-28

Query Match          51.6%; Score 297.5; DB 1; Length 252;
Best Local Similarity 59.8%; Pred. No. 2.4e-16;
Matches 64; Conservative 10; Mismatches 28; Indels 5; Gaps 4;

QY 3 LTQDPVSVVALGQTVRTITCGDLSLSYASWYQOK-PQAPVLVIYGNRPSGIPDRFS 61
.Db 148 LTPSSVSANLGTVEITVKTCGSGS-GSY-CWYQKSPGAPVTVIYNDKRPNSIPRFS 204
;
QY 62 GSSSGNTASLTITGAQAEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
.Db 205 GSKSGSANTLTITGVQVEADYVYCGSADNTN-AIFGAGTTLTVLG 250
;

RESULT 8
US-10-512-184-35
; Sequence 35, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

```

```

; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PLp9 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-35

Query Match          50.7%; Score 292; DB 1; Length 261;
Best Local Similarity 57.3%; Pred. No. 6.1e-16;
Matches 63; Conservative 12; Mismatches 29; Indels 6; Gaps 4;

QY 3 LTQDPVSVVALGQTVRTITCGDLS--LRSYASWYQOK-PQAPVLVIYGNRPSGIPDR 59
.Db 152 LTPSSVSANLGTVEITVKTCGSGSYAGSYGYGYYQKTPGSAFVTVIYNDKRPNSIPSR 211
;
QY 60 FSGSSGNTASLTITGAQAEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
.Db 212 FSGSLSGSTNTLTITGVQVDEAVYFCGAYDN--NYAGIFGAGTTLTVLG 259
;

RESULT 9
US-10-512-184-72
; Sequence 72, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising MBP - linker -
; OTHER INFORMATION: scFv PLp9.
US-10-512-184-72

Query Match          50.7%; Score 292; DB 1; Length 313;
Best Local Similarity 57.3%; Pred. No. 7.1e-16;
Matches 63; Conservative 12; Mismatches 29; Indels 6; Gaps 4;

QY 3 LTQDPVSVVALGQTVRTITCGDLS--LRSYASWYQOK-PQAPVLVIYGNRPSGIPDR 59
.Db 204 LTPSSVSANLGTVEITVKTCGSGSYAGSYGYGYYQKTPGSAFVTVIYNDKRPNSIPSR 263
;
QY 60 FSGSSGNTASLTITGAQAEADYYCNSRDSGNHV-VFGGQTKLTVLG 108
.Db 264 FSGSLSGSTNTLTITGVQVDEAVYFCGAYDN--NYAGIFGAGTTLTVLG 311
;

RESULT 10
US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

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; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-34

Query Match 43.1%; Score 248.5; DB 1; Length 259;
Best Local Similarity 45.9%; Pred. No. 8.1e-13;
Matches 51; Conservative 21; Mismatches 30; Indels 9; Gaps 3;
Qy 3 LTQDP-AVSVALGQTVRITCO-----GDSLSRYASYQQKPGQAPVLYYIGNRRPSG 55
Db 148 LTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSPKLLVYPASTRESG 207
Qy 56 IPDRFGSSSGNTASLTITGAQAEADYDNCNSRDSDGNHVVFGGKLTIV 106
Db 208 VPDRFIGSGGTDFTLTITSSVQAEADLADYFCQQHYST--PPTFGGKLEI 256

RESULT 15

US-10-512-184-71
; Sequence 71, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising ACE - linker -
; OTHER INFORMATION: scFv PL2.
US-10-512-184-71

Query Match 43.1%; Score 248.5; DB 1; Length 371;
Best Local Similarity 45.9%; Pred. No. 1.1e-12;
Matches 51; Conservative 21; Mismatches 30; Indels 9; Gaps 3;
Qy 3 LTQDP-AVSVALGQTVRITCO-----GDSLSRYASYQQKPGQAPVLYYIGNRRPSG 55
Db 260 LTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQSPKLLVYPASTRESG 319
Qy 56 IPDRFGSSSGNTASLTITGAQAEADYDNCNSRDSDGNHVVFGGKLTIV 106
Db 320 VPDRFIGSGGTDFTLTITSSVQAEADLADYFCQQHYST--PPTFGGKLEI 368

Search completed: November 18, 2005, 22:18:06
Job time : 2.40063 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:35:01 ; Search time 10.8549 Seconds
(without alignments)
983.894 Million cell updates/sec

Title: US-10-029-926D-7

Perfect score: 576

Sequence: 1 SEITQDPAVSVALGQTVRIT.....SGNHVRFSGTGKLTVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	97.9	109	2 S19663	Ig lambda chain V
2	558	96.9	108	2 S47184	Ig lambda chain V
3	547.5	95.1	110	2 S36272	Ig lambda chain V
4	542	94.1	127	2 S70444	Ig lambda chain pr
5	541	93.9	108	2 S38498	Ig lambda chain -
6	535	92.9	109	2 S38496	Ig lambda chain -
7	527	91.5	108	1 L3HUSH	Ig lambda chain V-
8	526	91.3	233	2 S25748	Ig lambda chain -
9	517.5	89.8	146	2 S02083	Ig lambda chain V-
10	514.5	89.3	110	2 S19672	Ig lambda chain V
11	499	86.6	96	2 S36060	Ig lambda chain -
12	498	86.6	115	2 S13726	Ig lambda chain V
13	498	86.5	233	2 S25741	Ig lambda chain -
14	438.5	76.1	106	2 S38495	Ig lambda chain -
15	420	72.9	105	2 S49533	anti-Sm antibody V
16	414	71.9	190	2 S25740	Ig lambda chain V
17	410	71.2	119	2 S30526	Ig lambda chain V
18	397	68.9	107	2 PC4283	anti-SS-A/Ro 60K p
19	395.5	68.7	120	2 S30525	Ig lambda chain V
20	384	66.7	226	2 S25745	Ig lambda chain -
21	381	66.1	231	2 S25751	Ig lambda chain -
22	381	66.1	231	2 S25738	Ig lambda chain -
23	376	65.3	120	2 S30527	Ig lambda chain V
24	376	65.3	151	2 S25739	Ig lambda chain -
25	376	65.3	231	2 S25753	Ig lambda chain -
26	374	64.9	233	2 S25747	Ig lambda chain -
27	373.5	64.8	212	2 S70431	Ig lambda chain -
28	370	64.2	107	1 L4HURL	Ig lambda chain V-
29	370	64.2	108	1 L5HUDL	Ig lambda chain V-

ALIGNMENTS

RESULT 1

S19663

Ig lambda chain V region (clone alpha-BSA3) - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C;Accession: S19663

R;Marks: J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A;Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on ph

A;Reference number: S19663; MUID:92085276; PMID:1748994

A;Accession: S19663

A;Molecule type: mRNA

A;Residues: 1-109 <MAR>

A;Cross-references: UNIPARC:UPI0000039C3B; EMBL:X61640; NID:929492; PIDN:CAA43821.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

P;15-89/Domain: immunoglobulin homology <IMM>

Query Match 97.9%; Score 564; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-41;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEITQDPAVSVALGQTVRITCGDLSRSYASVYQKPGQAPVLVIYKGNRPSGIPDRF 60

Db 2 SEITQDPAVSVALGQTVRITCGDLSRSYASVYQKPGQAPVLVIYKGNRPSGIPDRF 61

Qy 61 SGSSSGNTASLTITGAQAEADYYCNSRDSNGNHVVFVGGTKLTVLG 108

Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSNGNHVVFVGGTKLTVLG 109

RESULT 2

S47184

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

submitted to the EMBL Data Library, June 1994

A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien

A;Reference number: S47181

A;Accession: S47184

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-108 <MCI>

A;Cross-references: UNIPARC:UPI0000031AF6; EMBL:X79783; NID:9506426; PIDN:CAA56179.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

P;15-89/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 96.9%; Score 558; DB 2; Length 108;

Matches 100.0%; Pred. No. 5.3e-41;

	Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	SEITQDPAVSVALGQTVRIITCGDSLSRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF	60							
Db	2	SEITQDPAVSVALGQTVRIITCGDSLSRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF	61							
Qy	61	SGSSSGNTASLTITGAQAEADYYICNSRDSSGNHVVFGGQTKLTVL	107							
Db	62	SGSSSGNTASLTITGAQAEADYYICNSRDSSGNHVVFGGQTKLTVL	108							

RESULT 3

S36272
IG lambda chain V region (clone alpha-THY-29) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36272
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A>Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36272
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-110 <GRI>
A:Cross-references: UNIPARC:UPI0000118DP6; EMBL:Z18833; NID:G33419; PID:CAA79285.1; PID:CAA79285.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

		Query Match	95.1%	Score 547.5;	DB 2;	Length 110;
		Best Local Similarity	98.2%;	Pred. No.	4.3e-40;	
		Matches 107;	Conservative	1; Mismatches	0; Indels	1; Gaps
Qy	1	SETQDPAVSVALGQTVRITCGDSLSRYASWTQQKPGAPVLVIYGNRNPISGPDRF	60			
Dd	2	SELTQDPAVSVALGQTVRITCGDSLSRYASWTQQKPGAPVLVIYGNRNPISGPDRF	61			
Qy	61	SGSSGGNTASLITTCGAOAEADYYCNRSRSSN-HVVFGGGTKLTVLG	108			
			:			
Dd	62	SGSSGGNTASLITTCGAOAEADYYCNRSDDSNGLNVVVFGGTTKLTVLG	110			

RESULT 4

S70444
Ig lambda chain precursor V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
C/Accession: S70444; S70426
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A/Reference number: S70442; MUID:93024508; PMID:1383695
A/Accession: S70444
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-127 <CUI>
A/Cross-references: UNIPROT:Q9NSD6; UNIPARC:UPI00000176807
A/Experimental source: clone E29.1
R/Tonnelle, C.
submitted to the EMBL Data Library, May 1990
A/Reference number: S70426
A/Accession: S70426
A/Molecule type: mRNA
A/Residues: 1-90 <TON>
A/Cross-references: UNIPARC:UPI0000176808; EMBL:X53070
A/Experimental source: cell line E29.1, clone VL 29-1
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F/34-108/Domain: immunoglobulin homology <IMW>

Query Match	94.1%	Score 542;	DB 2;	Length 127;
Best Local Similarity	97.2%;	Pred. No. 1.5e-39;		
Matches 104; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	SELTQDPAVSVALGQTVRITCGDLSRSYASWYQQKPGQA	PVLVIYGNRRPSGIPDRF	60
Db	21	SELTQDPAVSVALGQTVRITCGDLSRSYASWYQQKPGQA	PVLVIYGNRRPSGIPDRF	80
Qy	61	SGSSSGNTASLTTGAQAEDEADYYCNSRDSNGHVVFGGTKLVTL	107	
Db	81	SGSSSGNTASLTTGAQAEDEADYYCNSRDSNGHVVFGTGKTIVL	127	

RESULT 5

S38498
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S38498
R/Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A/Description: Human antibody fragments specific for human blood group antigens from a phage library.
A/Reference number: S38488
A/Accession: S38498
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-108 <VAR>
A/Cross-references: UNIPARC:UPI000011554E; EMBL:Z23035; NID:g414043; PIDN:CBA80570.1; PII:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

	Query Match	93.9%	Score 541,	DB 2;	Length 108;
	Best Local Similarity	97.2%;	Pred. No. 1.5e-39;		
	Matches 105;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	SELTQDPAVSVALGQTVRTTCQDSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF	60		
Db	1	SELTQDPAVSVALGQTVRTTCQDSLSRSYASWYQKPGQAPVLVIYGNKRRPSGIPDRF	60		
Qy	61	SGSSSGNTASLTITGAQAEADYYCNSRDSNGHVVFGGTKTLVLG	108		
Db	61	SGSSSGNTASLTITGAQAEADYYCNSRDSINGHVVFGGTKTLVLG	108		

RESULT 6

S38496
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38496
R:Marks, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a p1
A:Reference number: S38488
A:Accession: S38496
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <MAR>
A:Cross-references: UNIPARC:UPT000011654A; EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match	92.98;	Score 535;	DB 2;	Length 109;
Best Local Similarity	93.5%;	Pred. NO. 5e-39;		
Matches 101;	Conservative 4;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	SELTQDPAVAVGALGQTVRIITCGDLSRLSYASWYQKPGQAPVLVIYKNNRPSGIDPRF	60	
Db	2	SELTQDPAVAVGALGQTVRIITCGDLSKYSYASWYQKPGQAPVLVIYKNNRPSGIDPRF	61	
Ov	61	SGSSSGNTASLITITGAQAEADYYNCNRDSSGNHVVFGGGKLTVLG	108	

Db 62 SGSPGNTASITITGAQAEADYICTSRDTSGNHVLFGGKTLTVLG 109
|||||

RESULT 7

L3HUSH
Ig lambda chain V-III region (Sh) - human
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C/Accession: A01980
R/Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A/Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete
A/Reference number: A92057; MUID:70166723; PMID:4909564
A/Accession: A01980
A/Molecule type: protein
A/Residues: 1-108 <TIT>
A/Cross-references: UNIPROT:P01714; UNIPARC:UPI0000012B9FC
A/Note: the sequence of the C region is also given
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:I19342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>
F:21-86/Disulfide bonds: #status experimental

Query Match 91.5%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 2.4e-38;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 1 SELTQDPAVSVALGQTVRITTCQGSLSRGYDAWTQKPGQAPLVLIYGRNRPSPGIPDRF 60
|||||
Qy 61 SGSSSGNTASITITGAQAEADYICNSRDSGNHVVFGGKTLTVLG 108
|||||
Db 61 SGSSSGHTASITITGAQAEADYICNSRDSGKHVLFGGKTLTVLG 108
|||||

RESULT 8

S25748
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25748
R/Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25748
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-233 <COM>
A/Cross-references: UNIPARC:UPI0000115EFC; EMBL:X57813; NID:933725; PIDN:CAA40950.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 91.3%; Score 526; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 6.1e-38;
Matches 99; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 21 SELTQDPAVSVALGQTVRITTCQGSLSRAYASWTQKPGQAPLVLIYGRNRPSPGIPDRF 80
|||||
Qy 61 SGSSSGNTASITITGAQAEADYICNSRDSGNHVVFGGKTLTVLG 108
|||||
Db 81 SGSSSGNTASPAITGAQAEADYICNSRDSGQVLFGGKTLTVLG 128
|||||

RESULT 9

S02083
Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N/Alternate names: amyloid-fibril protein GIL
C/Species: Homo sapiens (man)
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C/Accession: S02083
R/Fykse, E.M.; Sletten, K.; Huseby, G.; Cornwell III, G.G.
Biochem. J. 256, 973-980, 1988
A/Title: The primary structure of the variable region of an immunoglobulin IV light-chain
A/Reference number: S02083; MUID:89134210; PMID:3146981
A/Accession: S02083
A/Molecule type: protein
A/Residues: 1-70/71-72/73-75/76-131/132-146 <FYK>
A/Cross-references: UNIPARC:UPI0000176830; UNIPARC:UPI0000176831; UNIPARC:UPI0000176832;
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 517.5; DB 2; Length 146;
Best Local Similarity 91.7%; Pred. No. 2.1e-37;
Matches 99; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 1 SELTQDPAVSVALGQTVRITTCQGSLSLFNFVSWTQKPGQAPLVLIYKNNRPSGIPDRF 60
|||||
Qy 61 SGSSSGNTASITITGAQAEADYICNSRDSGN-HVFGGKTLTVL 107
|||||
Db 61 SGSSSGNTASITITGAQAEADYICNSRSGNYHVFGGKTLTVL 108
|||||

RESULT 10

S19672
Ig lambda chain V region (clone alpha-TEL14) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19672
R/Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A/Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on ph
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19672
A/Molecule type: mRNA
A/Residues: 1-110 <MAR>
A/Cross-references: UNIPARC:UPI0000115FE3; EMBL:X61644; NID:937856; PIDN:CAA43825.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 514.5; DB 2; Length 110;
Best Local Similarity 91.7%; Pred. No. 2.8e-37;
Matches 100; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 1 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPVLVIYKNNRPSGIPDRF 60
|||||
Db 2 SELTQDPAVSVALGQTVRITTCQGSLSRSYASWTQKPGQAPLVLIYGENRPSGIPDRF 61
|||||
Qy 61 SGSSSGNTASITITGAQAEADYICNSRDSGNH-VFGGKTLTVLG 108
|||||
Db 62 SGSSSGNTASITITGAQAEADYICNSRDSRGTHLEVFGGKTLTVLG 110
|||||

RESULT 11

S36060
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36060
R/Williams, S.C.
submitted to the EMBL Data Library, April 1993

A;Reference number: S36046
A;Accession: S36060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <WIL>
A;Cross-references: UNIPARC:UPI000011652D; EMBL:Z22202; NID:g312325; PIDN:CAA80211.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-85/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 499; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.2e-36;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60
|||||
Db 2 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 61
|||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNH 95
|||||
Db 62 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNH 96
|||||

RESULT 12
S31726
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S31726
R;Frippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 18, 7134, 1990
A;Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A;Reference number: S31726; MUID:91088295; PMID:2124677
A;Accession: S31726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-115 <PRI>
A;Cross-references: UNIPARC:UPI0000113BA7; EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PII
C;Genetics: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 499; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.2e-36;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60
|||||
Db 21 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 80
|||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNH 95
|||||
Db 81 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNH 115
|||||

RESULT 13
S25741
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25741
R;Combratio, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25741
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: UNIPARC:UPI0000115EF5; EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 498; DB 2; Length 233;
Best Local Similarity 86.9%; Pred. No. 1.5e-35;
Matches 93; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60
|||||
Db 21 SELTQDPVSVVALGQTLRIKCCQDTRSYASWYQKPGQAPVLLINGKDNRPSPDRF 80
|||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVFGGTXYLTVL 107
|||||
Db 81 SGSSSGNTASLTITGAQAEADYYCNSRDSSAHLVFGGTYLTVL 127
|||||

RESULT 14
S38495
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38495
R;Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pl
A;Reference number: S38488
A;Accession: S38495
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <MAR>
A;Cross-references: UNIPARC:UPI0000116548; EMBL:Z23029; NID:g414037; PIDN:CAA80564.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 438.5; DB 2; Length 106;
Best Local Similarity 78.7%; Pred. No. 8.4e-31;
Matches 85; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 1 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRF 60
|||||
Db 2 SELTQDPAVSVALGQTVRITCGDSLSRSYASWYQKPGQSPVLVFLDNKRPSGIPERF 61
|||||

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVFGGTXYLTVLG 108
|||||
Db 62 SGSSSGNTATLTITSETQAMDEADYFCQAWD---NGVIFGGTXYLTVLG 106
|||||

RESULT 15
S49533
anti-Sm antibody VL chain (V lambda 3b/J lambda 2/3) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C;Accession: S49533
R;Ahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-105 <NAH>
A;Cross-references: UNIPARC:UPI00001166FD; EMBL:Z46346; NID:g560845; PIDN:CAA86465.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;11-85/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 420; DB 2; Length 105;
Best Local Similarity 76.2%; Pred. No. 3.2e-29;
Matches 80; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 TQDPVSVSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLVIYKGNRPSGIPDRFSGS 63
|||||
Db 1 TQPPSVSVSGQTARITCGSDALPKQYAVWYQKPGQAPVLVIYKDSERPSGIPERFSGS 60
|||||

Qy 64 SSGNTASLITITGAQAEDEADYYCNSRDSNGNHVVFGGKLTVLG 108
| | | : | | | | | | | | | | : | | | | | | | | |
Db 61 SSGTTLTITISGVQAEDEADYYCQADSSGTYVVVFGGKLTVLG 105

Search completed: November 18, 2005, 21:47:21
Job time : 11.8549 secs

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RESULT 2

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LV3A_HUMAN
ID LV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70156723; PubMed=4909564;
RA Titani K., Wikier M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176 (1970).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01980; L3HUSH.
DR HSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
FT DOMAIN 1 97 Ig-like.
FT DISULFID 21 86
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11393 MW; E7E1229586411A56 CRC64;

Query Match 91.5%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 3e-44;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SELTQPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
Db 1 SELTQPAVSVALGQTVRITCGDLSRGLGYDAAYQKPGQAPLLVIYGRNRRPSGIPDRF 60

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLVIG 108
Db 61 SGSSSGHTASLTITGAQAEADYYCNSRDSGKHVLFGGTTKLVIG 108

RESULT 3
ID Q6GMW4_HUMAN PRELIMINARY; PRT; 233 AA.
AC Q6GMW4;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 03-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.S., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP NUCLEOTIDE SEQUENCE
TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073786; AAH73786.1; -, mRNA.
DR SMR; O6GMW4; 23-229.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5BD CRC64;

Query Match 91.3%; Score 526; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 9.1e-44;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 SELTQPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
Db 21 SELTQPAVSVALGQTVRITCGDLSRTYASWYQKPGQAPVLVIYAKDNRRSGVDRF 80

QY 61 SGSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLVIG 108
Db 81 SGSSSGHTASLTITGAQAEADYYCNSRDSGSHLVFGGTTKLVIG 128

RESULT 4
ID Q5NV73_HUMAN PRELIMINARY; PRT; 97 AA.
AC Q5NV73;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE V2-13 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```



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QY 19 ITQCGSLRSYASWTQKPGQAPVLVIYKNNRPSGIPDRFSGSSGNTASLTITGAQA 78
Db 1 ITQCGSLRSYASWTQKPGQAPVLVIYKNNRPSGIPDRFSGSSGNTASLTITGAQA 60
QY 79 EDEADYCNRSRDSGNHNVFG 99
Db 61 EDEADYCNRSRDSGNHNVFG 81

RESULT 7
ID Q8NSF4_HUMAN PRELIMINARY; PRT; 233 AA.
AC Q8NSF4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGLC1 protein.
GN Name=IGLC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3122211;
RA Darivach P., Lefranc G., Lefranc M.P.;
RT "Human immunoglobulin C lambda 6 gene encodes the Kern-Oz-lambda chain
RT and C lambda 4 and C lambda 5 are pseudogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:9074-9078(1987).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90324891; PubMed=2115572; DOI=10.1084/jem.172.2.609;
RA Vasicek T.J., Leder P.;
RT "Structure and expression of the human immunoglobulin lambda genes."
RL J. Exp. Med. 172:609-620(1990).
DR EMBL; BC032452; AAH32452.1; -; mRNA.
DR PIR; A39949; A39949.
DR PIR; S12441; S12441.
DR PIR; S12443; S12443.
DR HSSP; P01842; I1L1.
DR SNR; Q8NSF4; 20-229.
DR Ensembl; ENSG00000100208; Homo sapiens.
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;

Query Match 72.2%; Score 416; DB 2; Length 233;
Best Local Similarity 74.8%; Pred. NO. 6.9e-33;
Matches 80; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 2 ELTQDPVAVSVALGQTVRITCGDSLSRYASWTQKPGQAPVLVIYKNNRPSGIPDRFS 61
Db 22 ELTQDPFSVSVSPQATARTICSDGALPKYAYWYQKSGQTPVLVIYDDTERPSGIPDRFS 81
QY 62 GSSSGNTASLTITGAQAEADYCNRSRDSGNHNVFGGQTKLTVLG 108
Db 82 GSSSGTVA TLTLTSGAQVEADYCYSSDSGNNHNVFGGQTKLTVLG 128

RESULT 8
Q8FWF9_HUMAN PRELIMINARY; PRT; 232 AA.
AC Q8FWF9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RA Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089414; AAH89414.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 1.
```

```
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 24795 MW; F74218EFECFBCAC1 CRC64;

Query Match 66.4%; Score 382.5; DB 2; Length 232;
Best Local Similarity 71.0%; Pred. No. 1.4e-29;
Matches 76; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

Qy 2 ELTQDPVSVVAGQTVRTTCOGSLRSYASWYQKPGQAPVLVIYGNRPSGIPDRFS 61
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 22 DLTQPPSVSVSPGQTARITCGDALPRKYAPWYQKSGQAPVLVIYEDSKRPSGIPDRFS 81
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 62 GSSSGNTASLTITGAQAEADYYCNSRDSGNHVFVGGGKTLVLG 108
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 82 GSSSGTWTATLTISGAQVEDEGYCYSTDISG-YPVFGGKTVTLG 127
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 9
Q8N355_HUMAN PRELIMINARY; PRT; 234 AA.
ID Q8N355_HUMAN STANDARD; PRT; 111 AA.
AC Q8N355;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGLC1 protein.
GN Name=IGLC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RP Hughes-Jones N.C., Bye J.M., Beale D., Coadwell J.;
RX PubMed=2111699;
RA "Nucleotide sequences and three-dimensional modelling of the VH and VL
RT domains of two human monoclonal antibodies specific for the D antigen
RT of the human Rh-blood-group system.";
RL Biochem. J. 268:135-140 (1990).
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DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT BINDING 15 15 Ig-like.
FT BINDING 25 25 SCR3.
FT BINDING 29 29 SCR3.
FT BINDING 94 94 SCR3.
FT SITE 48 51 SCR3 binding.
FT DISULFID 21 86
FT NON_TER 111 111
FT STRAND 4 4
FT STRAND 8 8
FT TURN 13 14
FT STRAND 16 22
FT STRAND 32 37
FT TURN 38 40
FT STRAND 41 46
FT TURN 49 50
FT STRAND 54 54
FT TURN 55 55
FT TURN 58 59
FT STRAND 60 61
FT STRAND 64 65
FT TURN 66 67
FT STRAND 68 74
FT TURN 78 79
FT STRAND 82 88
FT TURN 91 93
FT STRAND 97 98
FT STRAND 102 104
FT TURN 107 108
SQ SEQUENCE 111 AA; 11935 MW; 69498EBEFD82053 CRC64;

Query Match 65.5%; Score 377; DB 1; Length 111;
Best Local Similarity 69.5%; Pred. No. 2.1e-29;
Matches 73; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 3 LTQDPVAVSVALGQTVRTICQDLSRYASYAWYQKPGQAPVLVIYGNKRRPSGIDPRFS 62
Db 3 LTQPPSVSVAAGTARITLCQDNGISGVHYQKPGQAPVLVIYFDRDRPSGIDPRFS 62

QY 63 SSSGNTASLTITGAQAEDEADYICNSRDSSGNHVVFGGTKLTVL 107
Db 63 SNSGNTATLTISRVEAGDEADYICQLWDSSEHVVFGGTKLTVL 107

RESULT 11
LV4C_HUMAN STANDARD; PRT; 107 AA.
AC P01717;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda chain V-IV region Hil.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=78187276; PubMed=418604;
RA Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
RT "Amino acid sequence of the variable region of the light (lambda)
RT chain from human myeloma cryoimmunoglobulin IgG Hil.";
RL Biochemistry 17:1718-1723(1978).
CC -1- MISCELLANEOUS: The sequence of the C region is apparently
CC identical with that of human SH lambda chain except in having 155-

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CC Ile (Hil numbering) instead of Val.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01983; L4HUHL.
CC HSSP; P01703; 7FAB.
CC SMR; P01717; 3-107.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; P:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT NON_TER 107 107 Ig-like.
FT SEQUENCE 107 AA; 11517 MW; A5C8AFFE0C0C590A CRC64;

Query Match 64.2%; Score 370; DB 1; Length 107;
Best Local Similarity 66.4%; Pred. No. 9.9e-29;
Matches 71; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 2 ELTQDPVAVSVALGQTVRTICQDLSRYASYAWYQKPGQAPVLVIYGNKRRPSGIDPRFS 61
Db 3 ELTQPPSVSVAAGTARITLCQDNGISGVHYQKPGQAPVLVIYFDRDRPSGIDPRFS 62

QY 62 GSSGNTASLTITGAQAEDEADYICNSRDSSGNHVVFGGTKLTVL 108
Db 63 SSTSGETVTITISGVQAEDEADYICQWDNSAS--IFGGTKLTVL 107

RESULT 12
LV5A_HUMAN STANDARD; PRT; 108 AA.
AC P01719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda chain V-V region DEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75112179; PubMed=4452363;
RA Bulitz M.;
RT "A new subgroup of human L-chains of the lambda-type. Primary
RT structure of Bence-Jones protein DEL.";
RL Eur. J. Biochem. 50:49-69(1974).
CC -1- MISCELLANEOUS: This is the first sequenced V region of lambda
CC chain subgroup V.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01985; L5HUHL.
CC HSSP; P06317; 1CD0.
CC SMR; P01719; 1-108.

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DR GO: 0005576; C:extracellular region; NAS.
DR GO: 0003823; F:antigen binding; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 97 Ig-like.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11343 MW; B8E8ED9C9C9E451 CRC64;

Query Match 64.2%; Score 370; DB 1; Length 108;
Best Local Similarity 67.0%; Pred. No. 1e-28;
Matches 71; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

Qy 3 LTQDPVSVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYYGNKRPSPGIPDRFSG 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LSQPPSVSVAPGQTARITCGDGIGKSVHWYQKPGQAPVLYVHEDNDRPAGIPERFSG 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 63 SSSGNTASLTITGAQAEADYYCNSRDSSGNHVFVGGGKLTVLG 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SMSGNTAALTISRVEAGDEADYYCEVWDDRTAHHVFGGGTKLTVLG 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
Q9UL82 HUMAN
ID Q9UL82 HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035032; AAD56268.1; -; mRNA.
DR HSP; P01703; 7PAB.
DR Ensembl; ENSG00000100208; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11445 MW; 52F0CC1AB26821DC CRC64;

Query Match 64.1%; Score 369.5; DB 2; Length 107;
Best Local Similarity 69.8%; Pred. No. 1.1e-28;
Matches 74; Conservative 8; Mismatches 23; Indels 1; Gaps 1;

Qy 2 ELTQDPVSVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYYGNKRPSPGIPDRPS 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ELTQPPSVSVAPGQTARITCGDGLLAKYARWFOQKPGQAPVLYFKDTERPSGIPERPS 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 GSSSGNTASLTITGAQAEADYYCNSRDSSGNHVFVGGGKLTVL 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GSSSGTAVLTITISGAQVEADYYCYSA-SUNNGRVFGGGTKLTVL 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
LV4A HUMAN
ID LV4A HUMAN STANDARD; PRT; 106 AA.
AC P01715;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda chain V-IV region Bau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75059189; PubMed=4435717;
RA Bacsko K., Braun D., Hilschmann N.;
RT "Pattern of antibody structure, the primary structure of monoclonal
   immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
   protein Bau.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:131-154 (1974).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01981; LAHUBU.
DR HSP; P01709; 2MCG.
DR SMR; P01715; 1-106.
DR Ensembl; ENSG00000100208; Homo sapiens.
DR GO: 0005576; C:extracellular region; NAS.
DR GO: 0003823; F:antigen binding; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 102 Ig-like.
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11306 MW; 4B6A688E0EC46571 CRC64;

Query Match 64.1%; Score 369; DB 1; Length 106;
Best Local Similarity 67.9%; Pred. No. 1.2e-28;
Matches 72; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

Qy 3 LTQDPVSVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYYGNKRPSPGIPDRFSG 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 LTQPPSVSVAPGQTARITCGDGLGEQVVCWYQKPGQAPVLYYHDSKRPSPGIPERFSG 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 63 SSSGNTASLTITGAQAEADYYCNSRDSSGNHVFVGGGKLTVLG 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SMSGTAVLTITISGAQDEADYYCQWDS--YTVIFGGGKLTVLG 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q5NV90 HUMAN
ID Q5NV90 HUMAN PRELIMINARY; PRT; 97 AA.
AC Q5NV90;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE V2-17 protein (Fragment).
GN Name=IGLV3-25; Synonyms=V2-17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
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